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(54) Title: HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW (57) Abstract This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.		

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HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW

This invention relates to new nucleic acid fragments encoding gene products or portions thereof, which fragments are obtainable from human nucleic acid populations, individual members of such populations being present in widely varying amounts.

5 Situations are increasingly arising in which it is necessary to study complex nucleic acid or polynucleotide populations. For example, it is now widely appreciated that an invaluable resource could be created if the entire sequence of the genomes of organisms such as man were determined and the information available. The magnitude of such a task should not, however, be underestimated. Thus, the human genome may
10 contain as many as 100,000 genes [a very substantial proportion of which may be expressed in the human brain (Sutcliffe, Ann. Rev. Neurosci. 11:157 (1988))]. Only a very small percentage of the stock of human genes has presently been explored, and this largely in a piecemeal and usually specifically targeted fashion.

15 There has been much public debate about the best means of approaching human genome sequencing. Brenner has argued (CIBA Foundation Symposium 149:6 (1990)) that efforts should be concentrated on cDNAs produced from reverse transcribed mRNAs rather than on genomic DNA. This is
20 primarily because most useful genetic information resides in the fraction of the genome which corresponds to mRNA, and this fraction is a very small part of the total (5% or less). Moreover, techniques for generating cDNAs are also well known. On the other hand, even supposing near perfect recovery of cDNAs corresponding to all expressed
25 mRNAs, some potentially useful information will be lost by the cDNA approach, including sequences responsible for control and regulation of genes. Nonetheless, the cDNA approach at least substantially reduces the inherent inefficiencies resulting from analysis of repeated sequences or non-coding sequences in an approach which depends upon
30 genomic DNA sequencing.

Recently, the results of a rapid method for identifying and characterising new cDNAs has been reported (Adams, M.D. et al., Science
35 252, 1991, pp 1651-1656). Essentially, a semi-automated sequence reader was used to produce a single read of sequence from one end of each of a number of cDNAs picked at random. It was shown, by comparing the nucleic acid sequences of the cDNAs (or the protein sequences produced by translating the nucleic acid sequence of the cDNAs) to each

other and to known sequences in public databases, that each of the cDNAs picked at random, could be unambiguously classified. The cDNAs could be classified as being either entirely new or as corresponding, to a greater or lesser extent, to a previously known sequence. cDNAs identified in this way were further characterised and found to be useful in a variety of standard applications, including physical mapping. Unfortunately, such a process is insufficient. The longer the process is pursued with any given population of cDNAs the less efficient it becomes and the lower the rate of identification of new clones. In essence, as the number of cDNAs which have already been picked rises, the probability of picking a particular cDNA more than once increases. This difficulty is exacerbated by the wide range of abundancies at which different cDNAs can occur, which abundancies can vary by several orders of magnitude. Thus, whereas some sequences are exceedingly rare, a single cDNA type may comprise as much as 10% of the population of cDNAs produced from a particular tissue (Lewin, B. Gene Expression, Vol. 2: Eukaryotic Chromosomes, 2nd ed., pp. 708-719. New York: Wiley, 1980). The need to avoid missing rarer species in any given population presents a considerable problem.

Various approaches (so-called "normalisation" techniques) have been tried in addressing the problem of increasing the efficiency of examination of a mixed nucleotide population, for example, such a population as is to be examined in human genome sequencing.

Thus, a standard PCR protocol can be used to amplify selectively cDNAs which are present at extremely low levels, if there is information about the sequence of those cDNAs. If not, a primer specific to the desired cDNA cannot be constructed and the desired cDNA cannot be selectively amplified. The standard PCR method is therefore inadequate if it is desired to characterise a number of unknown genes.

A second approach involves hybridization of cDNA to genomic DNA. At saturation, the cDNAs recovered from genomic/cDNA hybrids will be present in the same abundance as the genes encoding them. This will provide a much more homogenous population than the original cDNA library, but does not entirely solve the problem. In order to reach saturation in respect of the very rare sequences, it will be necessary to use huge quantities of cDNA, which need to be allowed to anneal to large amounts of genomic DNA over a considerable periods of time. Furthermore, cDNAs which are homologous to genes which are present in multiple copies in the genome will be over-represented.

A third approach exploits the second order reassociation kinetics of cDNA annealing to itself. After a long period of annealing, the cDNAs which remain single stranded will have nearly the same abundance, and can be recovered by standard PCR (see Patanjali, S.R. et al., PNAS USA 88, 1991, pp. 1943-1947; Ko, M.S.H., NAR 19, no.18, 1991, pp 5705-5711). The methods disclosed in these two publications, however, suffer from notable disadvantages. They are entirely dependent on the stringent physical separation of single stranded and double stranded DNA, require an elevated number of manual manipulations in each reaction, and necessitate protracted hybridisation times (up to 288 hours in the method of Patanjali et al.)

Yet a further approach in "normalising" a nucleotide population is described in co-pending British Patent Application No 91 15407.0, filed 17th July, 1991 by MRC, and involves a PCR process in which a mixture comprising a heterogenous DNA population and appropriate oligonucleotide primers is first formed and the DNA denatured, but before effecting a conventional PCR protocol the conditions are altered to allow the denatured strands of the more common DNA species to reanneal together, whilst avoiding annealing of primers to the DNA strands. By this means, rarer species can subsequently be amplified in preference to the more common species.

This PCR normalisation method in general comprises the steps of:

- (a) preparing a mixture comprising a heterogenous DNA population and oligonucleotide primers suitable for use in a PCR process, in which the DNA is denatured;
- (b) altering the conditions to allow the denatured strands of the more common DNA species to reanneal, while preventing the annealing to the primers to the DNA strands;
- (c) further altering the conditions of the mixture in order to allow the primers to anneal to the remaining single-stranded DNA comprising the rarer DNA species; and
- (d) carrying out an extension synthesis in the mixture produced in step (c).

Advantageously, the method consists of a cyclic application of the above four steps.

It will be appreciated that the conditions may be altered by the alteration of the temperature of the reaction mixture. However, any conditions which affect the hybridisation of complementary DNA strands to one another may be varied to achieve the required result.

5

Because the reannealing efficiency of any given DNA species will depend on the product of its concentration and time, the more abundant the sequence the greater the extent to which it will reanneal in any given time period. Once a DNA species has reached a certain threshold concentration it will no longer be amplified exponentially, as a significant amount will have annealed to the double stranded form before the priming step. Thus, as each individual DNA species is amplified by the process to its threshold concentration, the rate of amplification of that species will start to tail off. Eventually, therefore, all DNA species will be present at the same concentration.

15

The length of the reannealing step will determine how much DNA is present at the threshold concentration. Preferably, therefore, the duration of the reannealing step will be determined empirically for each DNA population.

20

In the PCR normalisation process in general, the DNA primers may be adapted to prime selectively a sample of the total DNA population. By using primers which will only prime a sample of the population, only that sample will be amplified and normalised. The total quantity of DNA generated will thereby be reduced, which means that the cycling times can be kept low. This ensures that the method is applicable to complex DNA populations such as cDNA populations. In addition, a first primer can be used which is adapted selectively to prime a sample of the total cDNA population, and a second primer which is a general primer. Advantageously, the general primer is oligo dT (each primed cDNA will then be replicated in its entirety, as the oligo dT primer will anneal to the poly-A tail at the end of the cDNA).

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In co-pending British Patent Application No 92 14873.3, filed by MRC 13th July, 1992, a new process is described which allows the study and identification of the individual members of a mixed or heterogenous population of nucleotide sequences perhaps of varying abundance. In preferred embodiments of the said process, the starting nucleic acid population is treated by:

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(a) subjecting the nucleic acid to the action of a reagent,

preferably an endonuclease which has its cleavage and recognition sites separated, which reagent cleaves the nucleic acid so as to produce double stranded cleavage products the individual strands of which overlap at cleaved ends to leave a single strand extending to a known extent;

(b) ligating the cleavage products from (a) with a population of adaptor molecules to generate adapted cleavage products, each of which adaptor molecules has a cleavage product end recognition sequence and the population thereof encompassing a range of adaptor molecules having recognition sequences complementary to a predetermined subset of the sequences of the cleavage-generated extending single strands; and

(c) selecting and separating only those adapted cleavage products resulting from (b) which carry an adaptor of predetermined recognition sequence.

A preferred endonuclease for use in step (a) of the above process is Fok I.

An important feature of this process is the use of adaptor molecules. The adaptors used must have "overhanging" fragment recognition sequences which reflect or are complementary to the extending cleavage-derived sequences which the adaptors are designed to react with. It is also preferred that the adaptors used should end with a 5' hydroxyl group. The avoidance of a 5' phosphate group removes the risk of inappropriate ligation involving the adaptors.

Adaptor molecules may also contain a portion permitting specific sequence selection and separation (as in step (c) of the process) when a sequence is attached to the adaptor. For example, an adaptor can carry biotin, thereby permitting advantage to be taken of the biotin/avidin

reaction in selecting and separating desired adapted molecules.

Additionally, adaptors preferably comprise a known and selected sequence such that specifically isolated adapted molecules can be amplified by known techniques (such as PCR) using a primer complementary to the core sequence.

Preferably the adaptors are short double-stranded oligonucleotides which can be joined to the ends of cleavage products. They will have been chemically synthesised so that their sequence can be predetermined

and so that large concentrations can be easily produced. They may also be chemically modified in a way which allows them to be easily purified during the process. As mentioned above, ideally their 5' ends will be unphosphorylated so that once joined to fragments the adapted end of the latter will no longer be able to participate in further ligation reactions.

It is preferred that the adaptor cleavage product end recognition sequences are on the 5' end of the longest oligonucleotide strand making up the preferred adaptor molecules, are at least 3 nucleotides in length and with totally random bases at the single-stranded position(s) two nucleotides in from the 5' end. This then allows selection to be performed both during the joining reaction and during subsequent priming reactions. Then, because the final degree of selection is a result of the product of the degrees of selection achieved at these two stages, maximum selection can be achieved per adaptor/primer available.

Adaptor strand extensions on the 5' end of the longest oligonucleotide also facilitate the use of modified oligonucleotides for separation purposes. Preferably, the short oligonucleotide will be modified at its 5' end. This has the double benefit of requiring just one modified oligonucleotide for all possible single-stranded extensions that are used, and also placing the modification at a position where it cannot interfere with ligation or subsequent priming reactions.

Although only one type of adaptor is required per ligation reaction, it is preferred that adaptors covering all possible reactions in a chosen subset of sequences be present, because then the opportunity for fragments in the chosen subset to ligate to each other is minimised. It is also preferred that the chosen specific adaptor, carrying a predetermined recognition sequence, should not only be different from the other adaptors in its single-stranded extension, but also different in the rest of its sequence since this allows orientation to be introduced which is useful in subsequent steps. It is therefore also preferred that this adaptor has a modified oligonucleotide to facilitate its separation with the cleaving products to which it joins.

The above "adapting" process can be used to generate categories or subsets of sequences by making some of the adaptors specific in some way, and selecting and separating as in step (c). In this way subsets of sequences can be provided depending upon the specific adaptor

chosen, e.g. for use in subsequent nucleotide sequencing. This facilitates, for example, the identification of a large population of sequences by permitting a rational approach to splitting such populations into subsets, each of which subsets can be examined in turn.

In the light of these developments, the present invention now provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-

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(a) a sequence selected from SEQ ID Nos 1 to 1193;

(b) an allelic variation of a sequence as defined in (a); or

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(c) a sequence complementary to (a) or (b).

In another aspect, the invention provides a nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof. Preferred sequences exhibit no more than 90% homology to a human sequence known per se.

20

In a further aspect, the invention provides a nucleic acid fragment comprising a portion of a sequence as defined above of sufficient size such that a probe of the same size and exhibiting complementarity to said portion can hybridise to said sequence. Preferably, such portions are at least 15 bases in length. It will be appreciated that minor mismatches in the aforesaid "complementarity" are not excluded provided hybridisation can still occur. In general, hybridisation conditions are within the choice of the skilled person, but reference can be made, for example, to the following: Melting temperature of hybrids - Bolton, E. T. and McCarthy, B. J. Proc. Natl. Acad. Sci, 48 p1390 (1962). Effect of formamide on lowering melting temperature - Casey, J. and Davidson, N., Nucleic Acids Res. 4, p1539 (1977). Effect of imperfect homology - Bonner, T. I. et al., J. Mol. Biol. 81, p123 (1973). General - Meinkoth, J. and Wahl, G. Anal. Biochem. 138, p267 (1984). Oligo hybridization and washing - Lathe, R. J. Mol. Biol. 183, P1 (1985).

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The present invention also envisages DNA constructs comprising fragments or sequences as referred to above with a control or regulatory sequence.

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The invention includes such DNA constructs using a gene system known in the art ligated to a sequence or fragment of the invention so as to enable, upon expression, the provision of a fusion polypeptide. Preferably, an endopeptidase recognition site is provided such that
5 when the sequence or fragment is expressed it is expressed in frame with a known protein with the boundary being a cleavage site for an endopeptidase with a rare cutting site. The known protein can then be affinity purified, and the peptide corresponding to the fragment or
10 sequence in accordance with the invention may be released by the endopeptidase. Alternatively, the whole protein can be used to raise antibodies which can then be screened for those directed at polypeptide corresponding to the fragment or sequence of the invention.

15 Since the present fragments and sequences can be used to produce, inter alia, corresponding genes, whether by isolating them, by synthesis or otherwise, such use and the resulting DNA fragments comprising genes are further aspects of the invention.

20 Yet another aspect of the invention is an expression vector comprising a fragment, sequence, gene-comprising DNA fragment, or DNA construct, as above, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory
25 sequence.

Other aspects of the invention are host cells incorporating a sequence, or fragment, or gene-comprising DNA fragment, or DNA construct, as above, as a heterologous part of the expressible genetic information of the cell. The production of such modified host cells can be achieved
30 using methods known in the art. Such modified host cells can be used to express corresponding proteins, and these materials lend themselves in turn to the preparation of corresponding monoclonal or polyclonal antibodies using standard techniques.

35 Also included in this invention are such antibodies. Reference can be made, inter alia, to the following literature: Monoclonal antibodies, Cambell, A. M. Laboratory Techniques in Biochemistry, and Molecular Biology Ed. Burdon, R. H. and van Knippenberg, P. H. vol 13. Elsevier Amsterdam 1984. Goding, J. W., Monoclonal antibodies: Principles and
40 Practice, 2nd Edition, academic Press, London 1986. Kipps, T. J. and Herzenberg, L. A., Handbook of Experimental Immunology : Applications of immunological methods in biomedical sciences, 4th edition Ed. Weir,

D. M. et al., p108 Blackwell scientific Publications, Oxford. Harlow, E and Lane, D. Antibodies, A Laboratory Manual, Cold spring harbor Laboratory, Cold Spring, New York.

5 Expression in an appropriate higher eucaryotic host may be important to ensure correct protein folding and also activity. Expression to avoid copurification of toxic products can sometimes be better performed in organisms approved for human consumption, eg prokaryotic *Bacillus subtilis*, eukaryotic yeast, mammalian cows milk vectors, and other
10 methods known in the art.

The invention also includes novel gene products or portions thereof encoded by a fragment, sequence or gene-comprising DNA fragment of the invention.

15

It will be appreciated that the sequences of the present invention collectively have utility based, inter alia, upon their common origin, and hence they can effectively be considered together rather than as separate entities. It is convenient to represent them as separate
20 sequences, because this is how they were produced and serves as "punctuation" between the different functional entities which each sequence represents. However, the sequences could just as easily have been presented as a continuous sequence derived by placing them end to end in the order in which they were produced, with a separate
25 indication of where the beginnings and ends of the component sequences are.

In contrast to investigations hitherto, where gene fragments (sequence fragments) could only be identified through some known characteristic
30 [for example: their homology to a fragment which largely encodes amino acids identified by sequencing a previously isolated peptide or is the antisense of that coding sequence; or them having at least partial homology to previously characterised nucleic acids; or them having ability to encode expressed proteins which could later be detected by
35 functional assays of the cells expressing those proteins or by using antibodies which had been previously raised against the proteins to detect their expression, Sambrook J., et al., Molecular Cloning CSH Press 1989], the sequences and fragments described by the present invention are entirely underivable and unpredictable from the prior
40 art, but are nonetheless clearly of great value for various purposes.

Thus, such sequences, by comparing them to sequence databases, can be

used as a means for determining the existence of new members of existing gene families, new human genes when previously only non-human genes were known and new genes when previously no genes were known (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1980)). In all cases, this allows the isolation of the corresponding genes and their products, and hence enables the manufacture of molecules of potential biological interest by recombinant means. Screening libraries of known materials or hitherto unexplored source materials for biological efficacy is now an important industrial activity in the search for new therapies and therapeutics. When new sequences have already been found to have counterparts in gene families or in non-human genes then knowledge about biological efficacy may already be apparent. For example, new receptors or receptor agonists/antagonists may exhibit differences to known instances of these molecules, and such differences could make them more suitable as therapeutics by, for example, exhibiting binding characteristics which are more in keeping with avoidance of toxicity. Reference can be made, for example, to polymorphic dopamine receptors and the implications for mental health (Iversen, L. Nature 358, p109 (1992), and Van Tol, H. M. et al., Nature 358, p149-152 (1992)). Where absolutely required, realisation of full length cDNAs for expression can be achieved by using the sequences to screen (by hybridisation) suitable cDNA libraries containing full length clones (D'Alession, J. M., et al., Focus (Gibco B.R.L) 9 pl (1987)). Alternatively, the sequences can be used to design primers suitable for obtaining the missing sequences by PCR or other amplification methods (Frohman, M. A., Dush, M. K. and Martin, G. R., Proc. Natl. Acad. Sci. 85 p8998-9002 (1988)).

Appropriate use of the sequence fragments in antisense or triple helix (Griffin et al., Science 245 p967-971 (1989)) applications will be useful for identifying manipulable targets related to disease. For example, viruses have been inhibited by antisense RNA to their mRNAs (Chang, L-J., and Stoltzfus, C. M. J. Virol. p921-974 (1987)). A similar effect could be achieved by targetting the expression of cellular proteins which are essential for growth or maintenance of the virus.

Partial or full length cDNAs have great utility once expressed. The manner of expression can be selected by one skilled in the art to suit the intended application. Expression of full length cDNAs is typically required for biological activity. Prokaryotic, and lower or higher eucaryotic hosts may be selected as the host for expression and higher

eucaryotes may be preferred to ensure correct modifications, for example, glycosylation in vivo, when this proves to be important. Expression can be ensured by situating the cDNA appropriately to signals for expression (Amann, E. and Brosius, J. *Gene* 40 p183 1985),
5 Shimuzu, Y et al., *Gene* 65, p141 (1988), Straus, D. and Gilbert, W. *Proc. Natl. Acad. Sci.* 82, p2014 (1985)). Such signals may include a promoter for transcription, which may itself be regulatable.

The proteins thus-expressed can be screened for activities of
10 therapeutic or commercial value. It may be that the proteins have to be first isolated for this purpose or can be assayed in situ. It may be desirable that some means of stabilising the expressed protein is employed. This can be achieved, for example, (and as indicated earlier) by expressing in frame as part of a fusion polypeptide (Smith,
15 D. B., et al., *Proc. Natl. Acad. Sci.* 83 p8073 (1986)).

Useful antibodies can be raised against the expressed proteins. It is commonly not an absolute requirement that full length proteins are produced, although this may influence the quality of the antibodies
20 produced. Peptides as short as 8 or 9 amino-acids in length can be used as antigens (Germain R., N. *Nature* 353 pp605-607 (1991), Rudensky, A., Y., et al., *Nature* 353 p622-627 (1991)). Immunogenic peptides could simply be synthesised using the amino-acid sequence translated from a sequence or fragment of this invention. It is desirable,
25 although not absolutely required, that some means of producing purified antibodies is adopted. When fusion polypeptides are used to raise antibodies, an affinity matrix specific for the generic part of the protein allows the fusion polypeptide to be immobilised (Smith, D. B., et al., *Proc. Natl. Acad. Sci.* 83 p8073 (1986)). The immobilised
30 polypeptide can then be used to affinity purify the antibodies. Antibodies to both the generic part of the fusion polypeptide and the part of interest are produced. When these need to be discriminated between, a different affinity column can be used to remove only those antibodies specific for the generic part of the polypeptide.
35 Alternatively, and as mentioned earlier, it can be arranged that the boundary between the two separate protein components of the fusion polypeptide has the recognition sequence for an endopeptidase with a rare cutting site. The peptide of interest can then be released from the affinity purified polypeptide by the action of the endopeptidase
40 (Nagai, K., and Thogersen, H., *C. Methods Enzymol.* 153 p461-481 (1987)). Another alternative is raise monoclonal antibodies against the purified protein.

The antibodies can be used for localising in situ, or quantifying in samples through, for example, ELISA or RIA assays, peptides against which they were raised. These uses are particularly beneficial when the results of the assays can be correlated to a disease condition, eg
5 cancer. For example tumour markers may be found and used to target therapeutic agents. The antibodies can also be used to detect or monitor markers of undifferentiated growth, infection, cardiovascular or immune disease or a therapeutic response. When the antibodies recognise cell surface proteins they can be used in isolation or in
10 combination to isolate particular populations of cells. These in turn can be used to isolate yet more cDNAs which will be enriched for yet more of such surface markers for the population, which, if similarly screened, will permit yet further subdivision of the population. Ultimately, panels of antibodies which can describe particular disease
15 states will accrue. Such antibodies could be tailored for forensic applications as well as diagnostic purposes and disease monitoring.

The sequences or fragments can also be used for genetic analysis and mapping, for example, to diagnose the likelihood that a given
20 individual is predisposed towards a given genetic disease. In the event of a sequence co-locating, genetically, with a disease gene, it can be used for the derivation of new disease therapies bases upon precise genetic knowledge. Such therapies can include, for example, the techniques of so-called "gene therapy" (Dusty Miller, A. Nature 357
25 p455-460 (1992)).

Antibodies can be produced against the protein of a genetic disease with sufficient discriminating power to discriminate between diseased and non-diseased states (Caskey, T. Genome Sequencing Conference,
30 Hilton Head, S. Carolina (1991)). This would be useful for reducing the dependence of such tests on nucleic acid-based screens. Such antibodies also have the advantage of allowing detection of faulty expression of the protein, for example levels of expression which may be important for development of the disease in slow onset conditions.

35 Also very important is that not all cDNAs are likely to be found by conventional means, whereas the present sequences are, in one sense, "comprehensive". The use of the class of cDNAs which corresponds of necessity to truncated clones increases the chances that part of a cDNA
40 will be cloned free of any sequences that could otherwise compromise it from being cloned. Sequence obtained can then be used to generate PCR primers from which the remainder can be obtained without having to

clone.

This invention will now be further described and illustrated by means of the following Examples.

5

All oligonucleotides used in these Examples were synthesised Trityl on using an ABI 380B DNA Synthesizer according to the manufacturers instructions. Purification was by reverse phase HPLC (see, for example, Becker, C., R., et al., J. Chromatography 326, p293-299 (1985)).

10

Example 1

Human brain and adrenal tissues were obtained from a mixture of 12 to 15 week menstrual age fetuses and then snap frozen in liquid nitrogen before storing in bijou bottles in a -80°C freezer. The two types of tissue were used separately, directly from the freezer, to prepare cDNA from which restriction fragments were generated for sorting into subsets. 1g portions of each of the separate tissues were homogenised, using an Ultra-Turrax T25 Disperser (Janke and Kunkel, IKA-Labortechnik), on ice in the presence of 4M guanidinium isothiocyanate to solubilise macromolecules. RNA was isolated from each homogenate by using centrifugation to sediment it through caesium trifluoroacetate. This was performed using the Pharmacia kit according to the manufacturer's instructions, except that centrifugation was performed for 36 hours and the RNA obtained was finally desalted and concentrated by performing two ethanol precipitations in succession with two 70% ethanol washes after each precipitation. In each case, polyA⁺ (mRNA) was isolated from 200 to 400 µg of the total RNA by binding it to magnetic oligo-dT coated beads (Dynal). Solution containing unbound material was removed from the beads, which were washed, and then mRNA eluted directly for use. mRNA isolation was performed in accordance with the manufacturer's instructions. Yields of RNA from the beads were between 1 and 3% of the total RNA. 2 to 4 µg of the eluted RNA were used for cDNA synthesis. cDNA synthesis was performed according to the method of Gubler, U and Hoffman, (B. J. Gene 25 p263 (1983)) using a Pharmacia kit according to the manufacturer's instructions. OligodT was used to prime the first strand cDNA synthesis reaction. The cDNA was purified by extracting twice with phenol/chloroform and then low molecular weight solutes including nucleic acids below ca. 300 bases were removed by passing the cDNA reaction mixture through a Pharmacia S400 spun column used according to the manufacturer's

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instructions. Running buffer for the column comprised 10 mM TrisHCl, 1 mM EDTA, 50 mM NaCl @ pH 7.5.

5 The column eluate was adjusted to 10 mM Mg^{2+} and then the purified cDNA was restricted by the action of 1 unit per 10 μ l of the endonuclease Fok I at 37°C for 1 hour, so that it would be able to accept adaptors to enable fragment sorting.

10 The cDNA fragments were purified by two successive phenol/chloroform extractions followed by passing them through S400 spun columns as described above.

The adaptors used were oligonucleotides 5' $N_4N_4N_4N_4$ TCCTTCTCCTGCGACAGACA (SEQ ID: 1194) with the complementary strand 5' TGTCTGTGCGAGGAGAAGGA (SEQ ID: 1195) and 5' AAN $_4$ N $_4$ TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1196) or 5' TTN $_4$ N $_4$ TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1197) each with the complementary 5' biotinylated strand GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198). These were added to 25% of the eluted material by incubating together 200 pmoles of the mixture of double-stranded adaptors in the elution buffer to which had been added MgCl₂ to 10mM, ATP to 10mM and 0.025 units/ μ l of T4 DNA ligase. The oligonucleotide 5' biotinylated GTTCTCGGAGCACTGTCCGAGA, (SEQ ID: 1198) and whichever of the complementary oligonucleotides with which it was used, each comprised 1/32 of the molar proportion total adaptors. The final reaction volume was 90 μ l which was heated to 65°C for 3 minutes and then cooled to room temperature before the ligase was added. Ligation was performed for 16 hours at 12°C.

30 Two successive phenol/chloroform extractions were performed to remove the ligase. The final aqueous phase was passed through an S400 spun column (Pharmacia) as described above except that the column was used with 10 mM Tris pH 8.3/50 mM NaCl.

35 The column eluate was adjusted to 25mM Mg^{2+} , 0.5mM dNTPs in a final volume of 200 μ l. The mixture was placed in a thermocycler (Techne MW2) and heated to 78°C for 5 minutes. At this point 10 units of cloned Taq DNA polymerase (AmpliTaq, Perkin Elmer) were added. This was followed by an incubation at 72°C for 10 minutes to fill in the unligated strand of the adaptor. After the second incubation 200 μ l of streptavidin coated magnetic beads (Dynal) prepared according to the manufacturers instructions were added to bind cDNA ligated to that of the oligonucleotides which was complementary to the 5'

GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198) biotinylated adaptor. Bead binding was allowed to proceed at 28°C for 30 minutes with mixing every 10 minutes.

5 Un-biotinylated cDNAs were washed from the beads with 400 µl each of 2M NaCl twice, fresh 0.15 mM NaOH four times at 28°C for 5 minutes each, water twice and finally a buffer comprising 20 mM Tris pH 8.3, 50 mM NaCl, and 25mM Mg²⁺. The beads were then resuspended in 240 µl of the final buffer including additionally 0.5 mM dNTPs and divided into 4x60
10 µl.

Four of the 60 µl aliquots, two from each tissue, were processed further specifically to prime and copy a subset of the immobilised, adapted fragments. 2 pmoles of the primer 5' CTGTCTGTGCGCAGGAGAAGGAA
15 (SEQ ID: 1201) were added to each of two aliquots, one from each tissue. 2 pmoles of the primer 5' CTGTCTGTGCGCAGGAGAAGGAG (SEQ ID: 1202) were added to each of the other two aliquots. 2.5 units of Taq DNA polymerase were added to each reaction and 16 cycles of alternate denaturation at 95°C for 30 seconds, annealing at 63°C for 2 minutes
20 and polymerisation at 72°C for 3 minutes was performed to accumulate the selected single-strands in solution.

On completion of the DNA synthesis reactions a further 30 µl of resuspended beads were added to each reaction to remove the
25 biotinylated fragments. The reaction was incubated at 28°C for 30 minutes mixing every 10 minutes to ensure that the biotinylated strands were bead bound. Each aqueous phase containing the newly synthesised strands was then removed and extracted with phenol/chloroform twice to remove the enzyme before being further purified by passing through an
30 S400 spun column equilibrated with 10 mM Tris pH 8.3/50 mM NaCl as described above.

Rounds of PCR amplification of subsets of the selected fragments were performed by using the original primer in each case, together with one
35 of the primers 5' GTTCTCGGAGCACTGTCCGAGAG (SEQ ID: 1199) or 5' GTTCTCGGAGCACTGTCCGAGAC (SEQ ID: 1200). This simultaneously rendered the fragments double-stranded and increased the amounts of available material. It was not known how many cycles of amplification would be required at this stage, since each primer pair would be expected to
40 behave differently. It was therefore necessary directly to determine a suitable number empirically by using standard agarose gel electrophoresis to examine the reaction products after a given number

of cycles. In some cases, to avoid the accumulation of non-specific products, it was necessary to perform an initial 5 cycles of amplification with both of the primers present at 2 pmoles each. All reactions were performed using 8 μ l or 12.5 μ l whichever was the larger but not exceeding 12 μ l of the column effluent above. Reaction conditions were adjusted to 20 mM Tris pH 8.3, 50 mM NaCl, 25mM Mg^{2+} , 0.5mM dNTPs and 2.5 units of Taq DNA polymerase in a final volume of 40 μ l. Apart from when an initial amplification with 2 pmoles of each primer was performed, 20 pmoles of each primer were used. Cycles of amplification were performed at 95°C for 30 seconds, 65°C for 1 minute and 72°C for 3 minutes.

For the purposes of cloning, selected cDNA was amplified as described immediately above, except that the reaction was not monitored. Instead, the number of cycles which had previously been shown to just give rise to all observable products plus another 4 cycles were performed. In addition, an extra 72°C for 10 minutes incubation was performed after the last cycle.

The products of the reaction were then prepared for directional cloning. Water was added to adjust the final reaction volume to 60 μ l. Enzyme was removed by two successive phenol/chloroform extractions. The final aqueous mixture was passed through an S400 column as described above, except that it had been equilibrated with 10 mM Tris HCl pH 7.5, 50mM NaCl.

For directional cloning, advantage was taken of the different known sequences introduced at each end of the selected cDNAs by the adaptors in a modification of the method of Aslandis, C. and de Jong, P. J. (Nucl. Acids Res. 18, p6156 (1990)). Different cohesive ends were produced on each end by using the exonuclease activity of T4 DNA polymerase to resect from the 3' end, to the first T in each case. To 75 μ l or 75 % of the column eluate, whichever was least, were added 9.5 μ l of 100mM TrisHCl pH7.4, 100 mM $MgCl_2$, and 9.5 μ l of 0.5 mM dTTP. 16 units of T4 DNA polymerase were added and the reaction incubated in a water bath at 37°C for 30 minutes. The enzyme was removed by extracting with phenol/chloroform, twice successively. The salt of the final aqueous phase was adjusted by passing it through an S300 column (Pharmacia) equilibrated with 10 mM TrisHCl pH 7.4, 1 mM EDTA as described above.

The E.coli plasmid cloning vector pBluescript KS+ (Älting-Meese, M. A.

and Short J. M., Nucl. Acids Res. 17 p9494) was prepared for accepting the resected cDNA by restriction cleavage at the BamHI and HindIII sites and then adaptor the resultant cohesive ends using the specific adaptors produced by the oligonucleotide 5' AGCTCGGCTCGAGTCTG (SEQ ID: 1203) with its partially complementary oligonucleotide 5' GCGACAGACAGCAGACTCGAGCCG (SEQ ID: 1204) and the oligonucleotide 5' GATCCGGCTCGAGT (SEQ ID: 1205) with its partially complementary oligonucleotide 5' CCGAGAACACTCGAGCCG (SEQ ID: 1206). Preparation of the vector and adaptor were performed according to standard procedures. Insertion of the cDNA was performed between the BamHI and HindIII restriction sites. Recombinant vectors were transformed into the host XL1-Blue (Bullock, W. O. et al Biotechniques 5 p376-378 (1987)) by the method of Hannahan, D. J. (Mol. Biol. 166 p577-580 (1983)). Suitable standard controls for the ligations and transformations were also included.

Post transformation procedures were as described in "Molecular Cloning", 2nd Edition (Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). Colonies were produced by plating onto X-gal/IPTG L-agar plates containing 50µg/ml ampicillin and 10µg/ml tetracyclin. Clear colonies were picked, each into a separate well of a microtitre plate, containing 100µl of L-broth and 50µg/ml ampicillin. Growth was allowed to occur for 16 hours at 37°C. 100µl of 50% or 30% glycerol was added to plates which were archived at -20°C or -80°C, respectively.

Bacteria corresponding to those archived were used for preparing templates for sequencing by the dideoxy method (Sanger, F. Milklen, S. and Coulson, A. R. Proc. Natl. Acad. Sci. 74 p5463-5467 (1977)). Bacteria for this purpose were either grown on L-agar plates containing 50µg/ml of ampicillin, prepared at the same time as they had been grown in liquid culture, or after plating out from the archive. Alternatively, fresh liquid cultures were inoculated from the archive.

In all cases, cDNA inserts were amplified for sequencing by PCR (Saiki, R. K. et al Science 239 p487-491 (1988)). PCR was either performed using bacteria directly added to the reaction, by a toothpick, or PCR was performed using 1/50th of the plasmid isolated by preparative methods (Holmes, D. S. and Quigley, M. Anal. Biochem. 114 p193 (1981)) from the bacteria in the liquid cultures or from the plates.

20 pmoles of each of the PCR primers 5' biotinylated GTAAACGACGGCCAGT

(SEQ ID: 1207) and 5' CGAGGTCGACGGTATCG (SEQ ID: 1208) were used in 40µl reactions containing 2.5mM Mg²⁺, 50 mM KCl, Tris-HCl pH 8.3 and 0.25 units of Amplitaq (Cetus). Reactions were performed at 95°C, for 1 minute, followed by 35 cycles at 95°C for 30 seconds, 60°C for 30 seconds and 72°C for 40 seconds. After the cycles, a final incubation at 72°C for 5 minutes was performed.

After PCR, standard agarose gel electrophoresis was used to determine which reactions had been successful. The biotinylated strands of successful reactions were then recovered for single-stranded sequencing by binding them to streptavidin coated beads (Dynal) and then washing, all according to the manufacturers instructions, except that the washing steps were either performed manually or performed automatically in the 96 well microtitre plate format using a Biomek robotic workstation attached to a side-arm loader (Beckman).

Dideoxy chain termination sequencing reactions were performed using the immobilised, biotinylated strands as templates and 2 pmoles of the oligonucleotide 5' CGAGGTCGACGGTATCG (SEQ ID: 1209) as primer. Reactions were performed using fluorescently-labelled terminators (Du Pont) or a fluoroscein-labelled primer (Pharmacia) according to the manufacturers instructions. Reactions were analysed using automated DNA sequencers. A Genesis 2000 was used for the "Du Pont" reactions and an A.L.F. for the "Pharmacia" reactions. Bases were assigned for the Genesis 2000 reads using the manufacturers Base Caller software. Files of called bases were then transferred to a SUN Network from an Apple Macintosh computer which had been used for base calling. Raw data from the A.L.F. reads was directly transferred to a SUN network where bases were called using the public domain "trace editor software" (TED). In both cases, files of called bases were entered into a Sybase™ database. Entering data entailed automatically removing vector and adaptor or linker sequences, but not editing ambiguous bases. After removal of the unwanted bases, files were automatically compared to other sequences in the cDNA database and the latest versions of the publically available databases, GENBANK and SWISSPROT. Searches were performed with the "basic local alignment search tool" (BLAST) (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1990)).

Sequences SEQ ID Nos 1 to 610, given hereinafter, were obtained by the above procedure.

Example 2

A second method of preparing cDNA libraries for obtaining gene fragments of the invention took advantage of the PCR normalisation process described above. Standard procedures were used to prepare mRNA from RNA that had been isolated by standard caesium chloride bouyant density gradient methods from a full term human placenta. The oligonucleotide LNotdt, sequence 5' TACGTTGACAAGCTTGAATTCGCGGCCGC(T)₂₆, (SEQ ID: 1210) was used at 1 μ M with AMV reverse transcriptase, to prime first strand cDNA synthesis under standard conditions from 0.5 μ g of the placental mRNA. Temperatures above 65°C were used to inactivate the reverse transcriptase and then the volume of the reaction made up to 100 μ l with water.

PCRs were then performed in reactions containing 1 μ l of the diluted cDNA, 10 mM Tris-HCl pH 8.3, 40 mM KCl, 1.5 mM MgCl₂, 0.01% gelatin, 200 μ M dNTPs, 10 uCi a³²P dCTP, 1 μ M each of the primers 11AD1, sequence 5' GCC(TA)(GC)CGCCGA (SEQ ID: 1211), and LNotdT and Taq DNA polymerase. An initial denaturation period of 95°C for 90 seconds was followed either by 35 cycles of standard PCR, comprising 95°C for 30 seconds, 45°C for 30 seconds and 72°C for 30 seconds or alternatively 3 cycles of the standard PCR already described followed by 27 cycles of Cot PCR during which an additional step of 72°C for 16 minutes was placed between all of the 95°C and 45°C steps of the standard PCR. The standard PCR was followed by a single 72°C for 3 minutes step while the Cot PCR was followed by one standard PCR cycle except that the 72°C incubation was performed for 3 minutes.

Products of the PCR reaction were end repaired by adding 5 units of T4 DNA polymerase to the reaction and then incubating at 37°C for 10 minutes. Enzymes were removed by phenol extraction. The cDNA was precipitated by 70% ethanol, dried and then resuspended in NotI buffer. 20 units of NotI were used to digest the cDNA under standard conditions. cDNA was again phenol extracted and ethanol precipitated. 10% of the purified NotI cut DNA were ligated to the vector pBluescript lting-Meese, M. A. and Short J. M. Nucl. Acid Res. 17 p9494 which had been prepared as standard to receive this DNA by restricting with the enzymes NotI and EcoRV. Transformation and processing of clear colonies was performed as described above except that the host E.coli strain DH5a was used in place of XL-1 Blue.

Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced were performed as described in Example 1.

Sequences SEQ ID Nos 611 to 772, given hereinafter, were obtained by the above procedure.

Example 3

5

cDNA libraries corresponding to adult brain cortex (Clontech Laboratories, Inc., Cat No. HL10036) and adult bone marrow (Clontech Laboratories, Inc., Cat No. HL10586) prepared in lambda gt11 phage were transfected into E.coli Y1090 and plated out for colour selection of recombinant plaques ("Molecular Cloning", 2nd Edition Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). 192 lambda Zap clones, corresponding to rhabdomyosarcoma cDNAs and a gift from C. Cooper, ICR, Sutton, were similarly plated except that the host XL-1 Blue was used.

15

Clear plaques from each library were resuspended in 5 μ l of Tris-HCl pH 8, 1 mM EDTA. 2 μ l of the resultant phage suspensions were added directly to PCRs for the purpose of amplifying the cDNA inserts for sequencing. PCR was performed as described in Example 1, except that the oligonucleotides used as primers for the lambda gt11 clones were 5' GGTGGCGACGACTCCTGGAGCCCG (SEQ ID: 1212) and 5' TTGACACCAGACCAACTGGTAATG (SEQ ID: 1213). Whichever of the oligonucleotides was to be used to prime the strand which would serve as the sequencing template was used in biotinylated form.

25

Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced was performed as described in Example 1, except that 2 pmoles of the primers that were unbiotinylated in the PCR were used as sequencing primers.

30

Sequences SEQ ID Nos 773 to 1193, given hereinafter, were obtained by the above procedure.

35

The following are the SEQUENCE LISTINGS which comprise sequences SEQ ID Nos 1 to 1213 referred to hereinbefore. Certain of these sequences are preferred, and are listed as such after the main SEQUENCE LISTINGS.

21

(1) GENERAL INFORMATION

(i) APPLICANT

(A) NAME: MEDICAL RESEARCH COUNCIL

5 (B) STREET: 20 PARK CRESCENT

(C) CITY: LONDON

(E) COUNTRY: ENGLAND

(F) POSTAL CODE: W1N 4AL

10 (ii) TITLE OF INVENTION: HUMAN GENOME SEQUENCES

(iii) NUMBER OF SEQUENCES: 1213

(iv) COMPUTER READABLE FORM:

15

(A) MEDIUM TYPE: DISKETTE

(B) COMPUTER: IBM PC COMPATIBLE

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: EXTRACT

20

(2) INFORMATION FOR SEQ ID :1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1:

GCCGATTCGT GACCAAGAAG GCTCTGTGCA TTCGGGTTTT CCAGGAGACT	50
35 CAAAAGCTGA AGAAGCGAAG AAGAGCCTTA AAGGCTGCAG CAGCAGCTCA	100
ATAACAAGC AAAGCGGAGG AACCCAGACA GCCCTTGTCC AAAGCCATAC	150
CAATATGATC TATCTTCTAA TGTATCCATG TTGTAATTAT ATATGTGTCT	200
40 GTGTGTGTCG AAATCTCTAG ACATACAGAT ATATATTCAT ATATCATATA	250

TATATATATA CACA

264

(2) INFORMATION FOR SEQ ID :2:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :2:

15

AGGAACATGT GTTTATTCAT CCAGCAGTGT TGCTCAGCTC CTACCTCTGT

50

GCCAGGGCAG CATTTTCATA TCCAAGATCA ATTCCCTCTC TCAGCACAGC

100

CTGGGGAGGG GGTCAATTGTT CTCT

124

20

(2) INFORMATION FOR SEQ ID :3:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :3:

ACAGAGCCGA TTCTGCATCC ACTGTGGTCA ACATTAGGA AGTTTAAAGC

50

35

TAAGATTTGC CAAATTGTAG CCTACTGGAT TCCGGTTCTC TTGACATCTC

100

TTTCTAGTAG CCATGTCTTG CACTTCCCGA GTATAACGA ACTGAGATGC

150

AAATTAAAAA AGGGAGGATT TAGAATAATG AAAAGAGAAA AGTCAAGAAA

200

40

GCACAATCAC TAGTGTAGAG ATAACAGAAT TTCTGAATTC CCTGAAAGCA

250

23

ATCTATATAA ATGCATGTGA AATAATACAC CAGCATCTGT GGGCCATACG 300

TCACATATTA GGAAGTATA ACATAAGGTA AAC 333

5 (2) INFORMATION FOR SEQ ID :4:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :4:

AGGGAGAAAG GAACATCCGC GAACAGCCAA AGAAATCTCA GAAGAGTCCC 50

GGAGCTCAAG GATCAGAGTA ACACAATTTT CACTTTTTCT GTCTTTATGT 100

20 AAGAAGAAAC TGCCTAGATG ACGGGGCCTC CTTCTTCAAA CAGGAATTTC 150

TGTTAGCAAT ATGTTAGCAA GAGAGGGCAC TCCCAGGCCC CTGCCCCCAT 200

25 (2) INFORMATION FOR SEQ ID :5:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :5:

ACAGAGCCAT TTGCATCCAC TGTGGTCAAC ATTTAGGAAG TTTTAAGCTA 50

AGATTGCCA AATTGTAGCC TACTGGATTC CGTTCTCTT GACATCTCTT 100

40 TCTAGTAGCC ATGTCTTGCA CTTCCCGAGT ATAAACGAAC TGAGATGCAA 150

24

ATTAAAAAAA GGGAGGATTT AAGAATAATG AAAAGAGAAA AATCAAGAAA 200

GCACAATCAC TAG 213

5 (2) INFORMATION FOR SEQ ID :6:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :6:

CGCAGGAGAA GGAACAGAGC CATTGTGCAT CCACTGTGGT CAACATTTAG 50

GAAGTTTTAA GCTAAGATTT GCCAAATTGT AGCCTACTGG ATTCCGGTTC 100

20 TCTTGACATC TCTTTCTAGT AGCCATGTCT TGCACTTCCC GAGTATAAAC 150

GAACTGAGAT GCAAATTAAA AAAAGGGAGG ATTTAGAATA ATGAAAAGAG 200

25 AAAAATCAAG AAAGCACAAT CACTAGTGTA GAGATAACAG AATTTCTGAA 250

TTCCCTGAAA CAATCTATAT AAATGCATGT GAAATAATAC ACCAGCATCT 300

GTGGCCCATATA CGTCACATAT TAGGAACTGA TAACATAAGG TAAAC 345

30

(2) INFORMATION FOR SEQ ID :7:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :7:

25

TCCATTTGAC ATCGCATTTT CATAGAAATG GCCAAAGAAA GAAGGTCCTG 50
GGGTTTTTTA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA 100
5 GCCCAATACA AAATATATAG AAAAAGCGAT TATTACAATA ACGCTTCAAT 150
TTCTTTTCC 159

(2) INFORMATION FOR SEQ ID :8:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :8:

20

ATATTTCAAT CGAACAAAAA GGAACTTTT TTTGAACTTA TTGAGGCTCT 50
ACTTAAGTAC ATCGAAACCC TTAATGCTTC TGGGGCTGTG TTGATTTCTT 100
25 TGCCTGGCTG GGGGTTTGAT TCGC 124

(2) INFORMATION FOR SEQ ID :9:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :9:

CCGATACAAA TGTACGGAAT GTGTGAGTCC CTCTGGGAGC CCAACATGGA 50
40 TCCGGATCAC CTGTTTGAAA CCATCTCCCA AGCCATGCTG AATGCTGTGG 100

26

ACCGGGATGC AGTGTGAGGC ATGGGAGTCA TTGTCCACAT CATCGAGAAG 150
GACAAAATCA CCACCAGGAC ACTGAAGGCC CGAATGGACT AACCTGTTC 200
5 CCAGAGCCCA CTATATATTA TTTCTACTTC ATCTATATAT TGCAAAAATA 250
GAAAATAGA 259

(2) INFORMATION FOR SEQ ID :10:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :10:

20

GTCACCAAGA CCGAGGCCAA ACTGGGCACC TTCCCAGGG CCCTCAAGAA 50
GCTCCTGCAC ACAATAAAG CGCCCTCGTT CTTTAGCAAG TCTGCTCCCT 100
25 CGAGGCCACA GCAAGCCGGC TACGGAGCCC CCGTTCTGTT TTGAGCCGAA 150
GACTACTTTA TTGGATGCGG TGAAAGGCCT CAGCTCTGAC ACTCTGATCA 200
CTGTGACAAG GGGCCC 216

30

(2) INFORMATION FOR SEQ ID :11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :11:

27

CACACTTCTT AAGATACATC AAGTACTAGT GATCTTTGCT AGCAGTTATG 50
 CCTGTTTCGT GTTACAGATT TGGCCATATA TTGACTAAAC AGCCCCTGTA 100
 5 AAGTTGAAAG AAAAAGTTTA TAACAGTGAA CTTCTGAGGT TTACGTTACT 150
 GCAGGCTTTG TTGAGAAGAG ATTGTTACAG TGTGATTTAT GGATGATCAG 200
 GGATG 205

10

(2) INFORMATION FOR SEQ ID :12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :12:

TGCATCTGAA GAGTTGATGA TCGAGACTAC AGCTGCACTA TCAGACTGTC 50
 25 AGGCAGCTCC CTCAGAAACA GCTTCAACAG ACTGGCTGCT GAGCAGACAT 100
 CACCGTCCTT CCGAGCTCCA CGGCGACTCC ACTCTCGAAC TTCAGTCGAA 150
 GTTGTTCCAC CACCTTCACG TTACCATTCA CCCTAAAAGA CCTTCTTGGG 200
 30 TAAGTCCATG CTGCGTCAAA TATTCCACTA TATTCCACAC TACTGCTGGA 250
 TATGCCATTG TCGGTGA 267

35

(2) INFORMATION FOR SEQ ID :13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :13:

GCCTCATCAG GTTTGCCCAG ATGCTGGAGA AGGTGTGCGT GGAGACGGTG 50
5 GAGAGTGGAG CCATGACCAA GGACCTGGCG GGCTGCATTC ACGGCCTCAG 100
CAATGTGAAG CTGAAC 116

10 (2) INFORMATION FOR SEQ ID :14:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 296 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :14:

TTCGAACTTA CCAGCATCAT GTTTGGTCTC TTCGTATGGT CAAACTTCAA 50
CTTTATAAAA ATAGTGAATA CCACTTATTG AGTGCTTAGA GTGTACCAGG 100
25 CATGGTGCTA AATACTCTCT ATCCATTATC TCATTAAATC ACATGACACT 150
ATGAGAAATG TACTATTCTT ATACCCACGT TGCCCAGGGT CATACTCTA 200
30 AGGGGTGCAA GGACCAGGCT TTGATTTCAT ATTATAATCT AATGCTCACT 250
CTCCAGGCCT GATGTCACGC AGCTCCTCAT TCTTATACTT AACATA 296

35 (2) INFORMATION FOR SEQ ID :15:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :15:

CGTCAGTGTG CTA CTT CACA TCATTAGCGA GGCC CAGAAA CTTGAACAGG 50
5 AAGTCCGGCA CTACCAACAT GCCGCCACTC ATACAACTCA ACTCTTCCTC 100
CAAAC TCGAT TCAAAGAGCA ATA 123

(2) INFORMATION FOR SEQ ID :16:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :16:

20

CAACACATTA GTGCATCAAT ATGAATTACT TGT TTTAAAAA ATCAAATGCT 50
GGCATTGTCA GAAAAATTA ACAGGTTTAT TTATAATTAT CATAAAGTTG 100
25 ACGCTGAAAC TTGTTCACTG AAACATTTTA ACTTGCATTA ATGCTTTACG 150
TCTCCGCATT TATATTAAAA ATTACACAC AAATGAAATG GAAAACTGC 200
CAATACCTGA TTTCTGTCCC TATTTTTCAC TCGCAATCAT ATACTTAGTA 250
30 CTTT TGA CTC TA 262

(2) INFORMATION FOR SEQ ID :17:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :17:

5 TAGCCAAATT CTAGGGCATC CAGATGCATT TGAGCCAGTC GTAATCCAGG 50
AAATGTCAAA AAAGCCCCAA TGAATGAACA GAAAATAGCC AGGAAAAATT 100
TGAAAGTAAG TTTTGAAACA GGA CTCTGG AGATTCTAAA CCTTGCATT 150
TCAAGAAACG TGCATCAGC 169

10

(2) INFORMATION FOR SEQ ID :18:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :18:

AGGGGCACCA TTACCATCCA TCTGACATCG CATTTCCATA GAAATGGCCA 50
25 AAGAAAGAAG GTCCTGGTAG GTTTTTCATA GAAAGACTCA AAAAGTTCAA 100
CCTTTGATGC TATGCCCCAG CCCAATACAA AACTACACAG AACAAAGCAA 150
TTATTAAAAT ACTGGCTTCG GTTCTTTTTT TTCCTTGCA AAGTTTCCTA 200
30 CATATATGTC TTTTACAGTA T 221

(2) INFORMATION FOR SEQ ID :19:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

31

(xi) SEQUENCE DESCRIPTION: SEQ ID :19:

TAGGCTCTGT GACGGCATAG TTTTCAGTAG CTTTATCACA ATATTCACAA 50
 5 TGGAGAATTA TATGACATGG TAGCAGAAAT AGGCCCTTTT ATGTGTTGCT 100
 TCTATTTTAC CTGAAATTGT AGATATAGGG TAATC 135

(2) INFORMATION FOR SEQ ID :20:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :20:

20

GTTATCTATC TATCTGCAG TTTACCTATC TGATCTGATC TCTGTAATTA 50
 TAGTTCTGTC ATTTAAAATA TACTATTTAA ATCTAATTTT TACATTTCAA 100
 25 AAATTATCTT CAGTAGTAAC TAAGTATATT TTCTGTGGAT TCTGAGAATG 150
 TTATTTTTC AATGTGAGA GTACATATGT ACATTTATAA TCTTGTGACT 200
 TTAAAGTCTG TTTTCAGATA CAGTATGTAA ATACTTGTA AAAAAATTGT 250
 30 ATAATTTTGT GATAATGTAG TTTCCCAAAA CACATTTAGA AAGCATTATG 300
 TTATTAGTAA ATGA 314

35

(2) INFORMATION FOR SEQ ID :21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :21:

5 TCTTCGCATC ACGCAGTACA GATACTCTTT CTGTACTTGC TTAATCTGCT 50
TTTTGGCATC AGTCAGTTCT CTTTCAGGTC AGCATAATCT TCTTCCTTCC 100
TCTGAAGATC TGCTTTCAGA TTCTGGGTAC GAGCAGAGCT TACAGAGAGT 150
10 TCCTCTTTCA ATATTTCTGT TTCTTGCC 178

(2) INFORMATION FOR SEQ ID :22:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :22:

ACATCTGATA TCCACCTCCA TGACAGACTG ATCACACCTC CTTCTATACT 50
25 ACTTCTGTTC TTTGTAAATA CTTAGTATTT TCCAAGGGAG TGTGAGAGAA 100
GAAATGCTAG GTTCATGAAG GGTCTCTAGG TTAAACTTTC TTTCTTTTTT 150
30 TTTCTTAAAA CAACACACTT ATTATCTTAC AAATCTGT 188

(2) INFORMATION FOR SEQ ID :23:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :23:

TTCCANCTAA ACATCCAATA TNCNTTTAN TGCTTTTATA TTTTNNAAAT 50
 5 GTTAAAACCC CTATACCACC TTTTGGGAAT GTTTTAAATT CTCCAATTTT 100
 TCGTTATATA GGATCAACCA ACTAAGAAAA GATTTTATCA ATTGAATTGA 150
 GG 152

10

(2) INFORMATION FOR SEQ ID :24:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :24:

ACAATACAGA GGACAAAGAC CCCTCACAGA ATGCTTTTCA ACCAACTTCA 50
 25 ACTTTTGCAC ACTTTTTCOA CGGTCCCACC ACA 83

(2) INFORMATION FOR SEQ ID :25:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 176 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :25:

AAATGTCCAT TGCTGTATTG CGTGACCGTG GTCCTTGCCT GTCAAATNCA 50
 40 ACAATGACCA AATGATGATG CGCCCTTAAT ACCAGGATGA GACCAAACCT 100

34

ACACATCTCC CAAGTGCCGA ACAAAAACCT GAACAAAAAC CATNTGCACC 150
CTACATCTGG CTGACATTTA CATTTT 176

5 (2) INFORMATION FOR SEQ ID :26:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :26:

AAATGTATGA TCAGAAATA GGTACGCTTT TAAAATATTT GAACAGAAAA 50
GCTACAAATA AATNGAGCAA TGCTTTTAAA ATCATCTTTG TTTTATAGAC 100
20 TTTTCTCGC ATGAATTACA TTTTACAATT TCATNNGGCA TATTCGCACT 150
TTAAGTACTG ACGAAGAAGA CTAAAACAAT CATTTTTTAA CAATATTTAA 200
25 AAGGATCATA TAGTCGACTT TTAAACANC CC 232

(2) INFORMATION FOR SEQ ID :27:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :27:

GAGAAAGTCC TTGCCATTCT AAAAGCCACC CCACTTCTCT AAGGAGAATG 50
40 GCCCAATCTT CCCAAGTCCA CACAGGAGGG AAACATTGTT TCGGTAAATA 100

35

CGCAATGCAA AATTTNNTAT CTTGGCTTAA TACNNCGACG TTTTATTTG 150

AATGATGAGC CTTCTGCCCC CCCTTCCCCT TTNNNCTCCC CC 192

5 (2) INFORMATION FOR SEQ ID :28:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :28:

TAACACTTTA ANCATCTCTC CAAGCCAAGG AGGCTATGAC ANTGTAGCTT 50

TTATACTGTC CCCATCGGCC ACAATAACAA ACTTTTAACC CTCATAAAAT 100

20 GAATGAAATC ATCTTTCTAA GAATCTATAC CTACAATTCT CTGAACTAAT 150

CAATGAAAAA GATGATCAAT TCTGACTAAC AAAGATATAT CGATTCCATT 200

25 T 201

(2) INFORMATION FOR SEQ ID :29:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :29:

AACCTAAGGC AGTTGACCCC ACCTTCCAAC ATGTTTTTAC TTTATTGGCC 50

40 CCTCCCTACA TTCGGGTTAG GTTCCATTTG ATTTGCACAA TAATGACTTT 100

36

. ATTTCTCTTT GATCAGGATT TGGCACATAA AATCCTTTTA TCATAGAACT 150
 AACTATTTTA ATTACATATA ATGTAATAA TGGAGAGATT TATAGAGAAT 200
 5 TTGTTTTTTT TGTCATATAC TCCATTTCGA AGACAGATAT GATAGAACTA 250
 GAAATTAAGT TGCATTCTG CAAGT 275

(2) INFORMATION FOR SEQ ID :30:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :30:

20

GTAAATNTAC AAAGATAACG TCGCAATTTT CTTAGATTTA AATCAAAGAC 50
 ATTCATCAAC AAGATTTCGA ATGGAATATT CCAGAAATTT CTGAGCCATC 100
 25 TGATCACAAC AACCGTCTTT GA 122

(2) INFORMATION FOR SEQ ID :31:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 197 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :31:

GGATTGNAG CTTGAAGTTC AGAGCTGGTT TACCCAAAAA GGGAGCCAAT 50
 40 AGAGATCTTC CCAATGAACC TCAATACACG ATCGTAATAC TCGCACAATG 100

37

AAATGTTAAG TATGATTCTA GACTTCACTG ACTATCACAA TGATATTTTC 150
TCGATCGCAC TAGTGCACAA CAAAACACGA TGAGTGCAAT GTGAAAC 197

5 (2) INFORMATION FOR SEQ ID :32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :32:

ACAAAAGTCT GAAGAAATCA CCAACNACAA GACGATTAGA AAATATGTTG 50
TTGGGGTCAC AACTAAAAG TCCCTGATCT ACATTGNNTT TCNACTC 97

20

(2) INFORMATION FOR SEQ ID :33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :33:

CAAATAAAAC AANTNTTGTA AAGCTACAAT AGTTATATAC CAAAGCAATA 50
35 CCTATTACAT GCTTTACACA ATCCCATGAA AAAATAATTT AATAGCTCCT 100
AATCCCTGAT GCAAGGCACT TCAAAGCACC CGCACAAAAC TCCATGAAAC 150
AACATACAAT ACATCATTTA AATAACATAA ACGACTTTCA CACACTTGAC 200
40 CTAGGAAAAA ATAAATCCA TACAACCACA GCTAAAAACA TGTTAAGATT 250

CACAATAAGA

260

(2) INFORMATION FOR SEQ ID :34:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :34:

15 GGACNTGCGC NNNANNNANA GCCANTGAAC NCAGCCACCA NTGCAAGAAG 50
ACTGCCTCTT NCCAGGCAAG ATTTTACTGG AGCAACANAA CCGGAGGTGT 100
GATCCAAAAT ACCTTCCTTN CCAAGCCCCG GGTNNNNGAT AAGGTGTGGA 150
20 NTTNGGTTAA AGACAAGG 168

(2) INFORMATION FOR SEQ ID :35:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :35:

35 CTCGNACACT GTGGAGAGCC TGCGNNNNNN NNGGTNTACT CAGGGGGACG 50
AAAAGGAGNN GAANAAGTGA CACNGCNGNT AGCAGAGNGC ACAGAGCTGT 100
GCTNNNGTGG TCCCTTAGNA CCCGAGNAGG TGGGCGCGAG GTGAANAAGG 150
40 TGCNNGTGCG AGAGTGCGTG ATT 173

39

(2) INFORMATION FOR SEQ ID :36:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :36:

AGCAAGTNNN NNNNNNCATC CTGAAAGTCA AAATGGAATT TGTGTTTATA 50
15 CAACTAATAA TGATTTTTAT TTGCTCAGTA CAGACTNATT TACAATGAAA 100
GTTTTGCTAA CCTTGGTAAG CTTGTTTACC GTTT 134

(2) INFORMATION FOR SEQ ID :37:

20

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :37:

30

TGGCGCCTGT CCGAGAGCAA GTNGNNNNNN NNCCTGAAAG TCAAAATGGA 50
ATTTGTGTTT ATACAACTAA TAATGACCTT TTATTTGCTC AGTACAGACN 100
35 GATTTACAAT GAAAGTTTTG CTAACCTTGG TAAGCTTGTT AACCGTTTAC 150
ATGACTTCTT 160

(2) INFORMATION FOR SEQ ID :38:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs

40

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :38:

CTAGTTTAAT GAATCTGAGG GGCTACTATA AACAAATCCCA CCCTCACACG 50
ATTTTTTACC TTCNTTACTT NGCCCTTCAT TAGGCAACCC TAGCAGCACT 100
CCACCTCTAT TCTCGCACTG TCCAAGAGGC CCACCTAATC 140

15

(2) INFORMATION FOR SEQ ID :39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :39:

AGCAAGTATC ANNNNNNNNN ATACATTGGA ATTCAAGTTG TTTTGTGTCA 50
AATTGTACAG TGTGTCAATT GATCTTCAAG CTGNNGGTGC CTAGAAATGG 100
GNCGGTGTCT GTAGCCCTGG CATGTGCACA CGGAGCATTT GCCACCACCG 150
CAAGCAAAAA GTCTGGGNGA AGTTCACCAA NGNCAAGAAN NATTANGGGA 200
AAA 203

35

(2) INFORMATION FOR SEQ ID :40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

41

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :40:

GAAAAGCNNN NNNNNNNGGC TTAAAGAACA ATATGCTGAG ATGGAGAAGG 50
ACCTAGCGAA ANTNNNAACC TTTTAAGAAC TTGAANNACA ACAATCACAA 100
10 ACTAATGAGA AGATGTTTAC CTCTCTCCTG AAAACTATGC CCACCAGACC 150
GTTTAGCCTC TGCTCAAGCT 170

15 (2) INFORMATION FOR SEQ ID :41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :41:

GCTGCATGTT TCCTTGNATT TGAGCTTGAA AGTTCAGAGC TGTTTACCCA 50
AAAAGGGAGC CAATAGAGAT CTTCCCAATG AACCTCAAAC ACGTCGTAAT 100
30 ACTCGCACAA TGAAATGTCA AGTATGATTG TAGACTTCAC TGACTCATCA 150
CAATGATATT TTCTCGATCG CACTAGGCAC AACAAAATAC GATGAGTGCA 200
35 ATGTGAAACA TCTACAAAGT AAATCACACA CTGTTTTTTT AAATNCATAG 250
AAATTTGATT TGTAATAAAA 270

(2) INFORMATION FOR SEQ ID :42:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

42

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :42:

10	AGAGCTGCAT GTTTCCTTGA TTTGNAGCTT GAAGTTCAGA GCTGTTTACC	50
	CAAAAAGGGA GCCAATAGAG ATCTTCCCAA CGAACCTCAA TAACGATCGT	100
	AATACTCGAC AATGAAATGT TAAGTATGAT TCTAGACTTC ACTGACTATC	150
15	ACAATGATAT TTTCTCGGAA TCGCACTAGT GCACAACAAA ATAGATGAGT	200
	GCAATGTGAA ACAATCTCAA AGTAAATCAT ATACTTGTTT TCTTA	245

(2) INFORMATION FOR SEQ ID :43:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :43:

30

	TACTGNGA AAATGTACAA AGAAAGTATC CCCAAATNAT TTACAAAGCC	50
	TAAATGTCCT TGATACACAT ACACGGNAGT ATGCAGACAA CAAAGATTAA	100
35	ATGAAGACAC TTTACACTTT TCGG	124

(2) INFORMATION FOR SEQ ID :44:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

43

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :44:

GAGTTCTCAC GAATACACAG GTTCAGAGAG ATGAGANGGA ANAACATAAG 50

GCAAATTCCT AACANNCGCT AATATAGGAG GCCGCTCGAT AGGATTTTAA 100

10

AAAAATAAAA ACAATCTTAA TAGTGGGACA AGGCCATCAG AAAA 144

(2) INFORMATION FOR SEQ ID :45:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :45:

25 ACTGATTCNN NNTGAAAATA CCCCCTTTCT CCATTAGTGG CATGCTCATT 50

CAGCTCTTAT CTTTATATTC CAGTAAGTTA TTTTGCTCTC ACTGTTTTAA 100

CAAAAAAAAA AACACAACA TAAAATCCT TGCAAACCAT GTCAATTGGA 150

30

GAAATTTAAT GTTTTTCATA ACATGAA 177

(2) INFORMATION FOR SEQ ID :46:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :46:

ACTGATTCTG CGAAAATACC CCCTTTTAT TAGTGGCATG CTCATTCACT 50
 5 TTATCTTTAT ATTCAAATAA GTTATTTTCGC TTTCACGTGTT TTAACAAAAA 100
 AAAAAAAAAA AAAAAAATAC AGCCCTCCCC AATCGAAGAT TTCAACTTTT 150
 TAATTCACAC GGAAAAACCA AGACAATTTT ACAACTTCTG GACACAACCA 200
 10 TCAACACAGG ACATTTTTTTT TACAGGCAAA TCACTTAAAA CAAAAAAGAT 250
 CCCAGA 256

15 (2) INFORMATION FOR SEQ ID :47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :47:

GAGAAAAGTC NNNNNNNNNA GGTAAATCTA ACTTTTCTTG CTTATTTTCAG 50
 CTATGATCTG AAAGGATGGA AGACACAAAA TGTATGNNTA AGGTATTTTT 100
 30 AACAAAGATA CATGGGTAAA TTAACAGCAG TAATGTAAAA AAGACTGAGG 150
 AGCAA 155

35 (2) INFORMATION FOR SEQ ID :48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :48:

5 GCTTATTTTA CTATATCTAA AGGATAAAGC ACAAATGAT GAATAAGATA 50
TTTNNACAAA GATACACG 68

(2) INFORMATION FOR SEQ ID :49:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :49:

20 CCTGAAAGCA AAGCCATNNA AAGCTTAGAG ACAAGCACNT GAGATGCAGG 50
GGCCTAGCTA AATTTNGAAC CTGNTGGAAC TTGAACCACA ACGATAAAAA 100
ATTACAGAAG AGTTCACCTC TTTCTGAAAA CTATCCACAG ACCGTTTACC 150
25 TCTGCTTCAA GCTANCAATA TATCAATGGC ACTCTCATAN CAGAAGAAAG 200
AAGTTCCTAC TAGCTCCTGA TTATATTNAA GAAGATGCCC ATGG 244

30 (2) INFORMATION FOR SEQ ID :50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :50:

ACTCGNNCAG CGATAGTCGG AGCTCACCAA CAAAAACNCT NNNNCAGAAA 50

46

GGANAAAGNG CCGCCCTACG TGGTACACAC A

81

(2) INFORMATION FOR SEQ ID :51:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :51:

15 GTACTTACTG CACTATGAAA AGCAATAGAT CGTCCATAAG TTATAACCAA 50
AATCTCTCCC TCAGGAATAT ATTCCATACT ACTAACAGAC ATATTAAAAT 100
TTAGAGATTT CACTTCTGTC ATAGTAGCAT GATCCCAAAG TCGAACAGTT 150
20 TTGTCATCAG CAGAAAGAAT CTGTTTATCT CACTGCACCA CAGAGCTTTT 200
TTATACCAGA AGNATGACCA CTG 223

25 (2) INFORMATION FOR SEQ ID :52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :52:

TATGGTTTNT TGTA AAAAAG CTCANNNANA AAGGGANNNGG CTTAAGAGA 49

(2) INFORMATION FOR SEQ ID :53:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs

47

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :53:

CAACGTCAGA GCACACNNNN NNCTCAGNGC ANAGGCATGA CAGGAGCTCA	50
TANCNATAAG CCATATAANN NTGTTACCTG TATAGAATGA TGAATTATCT	100
TTCTAGAGTC TATACCTACA GTTCTCTGAG CTAATCAATG GAAAAGATGA	150
TCAATCTGAC TAACAAGAGN AATTGATTCA TTTTCTTCCA CNCCCCTTCA	200
TTCAATAATC AAA	213

20

(2) INFORMATION FOR SEQ ID :54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :54:

30

GCGTGTTGTG NGGAGTGGNN GTCTNGTCNT CCTGTTAAGG TTTTGTGTG	50
CGTNNTTGCG TANGGGGNGG GTTTNGGCAG GTGTTGCCGG TAGCNAAACN	100
GTTGGCCCCA TNGCCNGNAT TGNNNCCCN CNNGGGAANG GGGGGGNGA	150
CCNNAGNGGG AAAAAA	166

35

(2) INFORMATION FOR SEQ ID :55:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs

48

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: doubl
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :55:

ACCTCATAGC GAACTCGTCN TATAGANNNN ANNTGAGTCG AGCTCGATGT 50
10 NGNCGTTGTN GCTGCCAAGC GACAT 75

(2) INFORMATION FOR SEQ ID :56:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :56:

25 AATNNNNNCC TATTTTGTA TTTTTTGAA AAAAGTTCAA TGTTCAAGTT 50
TCCTTAGTTT TTACCTTGTT TTCTCTATAG GTCATGATTT CTGTGAAGCA 100
AAAAGATGCC TTTTACCATG AATTCTTGAG TTTACATCAA TAATATTGTA 150
30 TATTAAGGGG ATCAGAAGTA GGAAGGAAAA A 181

(2) INFORMATION FOR SEQ ID :57:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :57:

TCGAAGAGAC CTCAATCACC GTTTTTCAGG ATGTTTGATC ACAATACGAA 50
5 GATGACGNN A TCCAATTTC GAACACCACA GGGCACTGGC ACACAGAGGG 100
GATTATTACA GAACCACTGA GATGACATTT 130

(2) INFORMATION FOR SEQ ID :58:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :58:

20

GTNATTTTGA AGGTCTCACA AATNTAAAGA CTTATTGTAG CCCATGAACA 50
CATTGACAAG TACAAAATT ACAAAAATAT GCAGAAATAT TGAATAACTA 100
25 GAACACAAGC CACTGTTTCA ACTCCAGAAA AAAGAAAGGC TTTACTTTTT 150
CCATGAA 157

(2) INFORMATION FOR SEQ ID :59:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :59:

40

GAGGTGAAGT TGTTCCTTAT TGAATTGCAT TATNAATGNA TAGGCTGTGC 50

50

CTTTTGNAC TCTCTATGAG TTCATGAATT TAACCAATAC GNCCACAAAT 100
GCTGCTGCTG TCACAGAGAG ATGCCGATAA AGGACACCCA CCACCAATTT 150
5 TTGAACAGGG AGGGGAGAAT CAACTCTGAA TGTGATGCAG TGACCAGGAG 200
AGAGGACCAT GTTAACAACA CCACACAAAT GCAAATGACT NGTTCTNAAA 250
CA 252

10

(2) INFORMATION FOR SEQ ID :60:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :60:

GACCTCGTTT TTCATCCTAT TATGGCGTTT ANCAGGCTAG ACAGAAACAC 50
25 GCCTTAACTT TANTTGCCAC AAATCTTAAT ATTTTCTCCA CTAATATTAG 100
AAAGGAAGCA ACAAATAATG TCGCTTTTCA CCTGACGTCT GGTTCAACTT 150
TCCGCCCAGC CTATTCCTGN GTCTTCCTCC TGCCTTTCTA ATGTCCCA 198

30

(2) INFORMATION FOR SEQ ID :61:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :61:

51

GAGGTGGCAT TATGTGAGAC AGCATTTGGT TAGGGAGTGC CAAGCATTCT 50
ACAGCATTG ATGGTGGAAG TAGTCATGCT TTTTATTTCT GCTCTCTAGG 100
5 AATGTAAGGT GCACAGCAGG TCAGGGTACT GCTGTGTGAG ACAAAGGTC 150
CAGGTAGAGG CAATCCCCA GATGCAGGCA GGGCAGGTGC TCACTGGGCA 200
GAGTGCTTCT CATAACCTT CAGGAACCC 229

10

(2) INFORMATION FOR SEQ ID :62:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :62:

CATCCTGGGC CCTGGCCGAT GTGCATATCA ACANAAAAA GGGACTGAAG 50
25 AACATCGGCC ATATCATCCA CACAAGCCAA ATCTCACACC TTTACTTTAA 100
ACCGCTTAAT GAATTCATG ACCTTGAGGG CTAAAGATCG TTCTTCGGGC 150
AAGAGCTTTT GGACTGTTTT TAGAACAGAA T 181

30

(2) INFORMATION FOR SEQ ID :63:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :63:

52

5 GTTGATTGTG AATCATCCCT CTAACATATA ATCAANANTA TGAGTAGAGA 50
ATTGGCAGA AACAAGAAAA GGACATGGGA TAACTTTTAG ATTAAAGAG 100
GCAGGCTTGG AACACAAACT GGTATTCTGC TGACACACTG CTGCATATCA 150
TAAGGCTACT CCACAAGACC ATTAGAAGTC 180

(2) INFORMATION FOR SEQ ID :64:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :64:

20

ACAATGTTCC AACATATATA TGGGGAGGGG AGAACANTTA TCTGTATAAC 50
AGGGAAGTGT GATTATTTAA AAATANGCNA GAACTTATTT CANCTGTGCT 100
TTAGAAANAA NTGTATACGG 120

25

(2) INFORMATION FOR SEQ ID :65:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :65:

40

CACATCGCTA TAATCCTTTC TGAGGACTTA AAACCTTATN CCACTTACCT 50
TTATGACTTT TAACAAGCCT 70

(2) INFORMATION FOR SEQ ID :66:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :66:

TTTCGAGCAA AATGTTTACA TTTACATGGA AATACACACT AAAACAGAAT 50
15 ATTTTCCTAA TCATGAAACT TCGCCAAAGC AAAATACAAA CTTCCAACGG 100
GAGGTCCACT CAACTAACAA CAATGATCCC CAAGCAGGGC ACCAAGAAAC 150
CTGGGGGACC CTTTNCAAAA AACCTCCTTT CAAGAGACCC TAATACTCTN 200
20 TCCACACACC CACACGATTT AGGAACTTGG ACATGTTTCCT 240

(2) INFORMATION FOR SEQ ID :67:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :67:

35 GGAAGCACTA CATTTTCATCC AAAGCTGGGT TGAGTTATTT TTGAACACTT 50
TAGGATATGC TTAGGTAGGC TTTTAACTTG CTCCTCCAAA CAATATCTNT 100
TGGGAAAACA AGCCCTGTGG AGAGATCCTT CCATCAAGTC GCTTCAATTT 150
40 AACCTATTTC TAGAGGACTA GACATGCAGA ATCGTCAACT ACAGGGAATG 200

AAAAGTTCAA AAAGTAGATC CTACAAGATG AACGAGTACT TTTCTAAACA 250
TAAG 254

5 (2) INFORMATION FOR SEQ ID :68:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :68:

AGGCACCAAA GAAACACCAA GCAATAAAGT GAAAGACTAA CCAAGATTTG 50
ACATTGTATG NTTACTGTAT TCTTTAAGAA ACAACTACAA AAAGAAAATG 100
20 TCAACAAATN NNNACAACCTG AGAACCTGGG AATTCCCGCA CGGAAGACAA 150
GAGATAACCT CTCCAATTTA ACACCGCTAG GNTTCTATNN TA 192

25 (2) INFORMATION FOR SEQ ID :69:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :69:

AGCAGCGNNN NNNNTNNAAG CAAAAGACAG GAGCAGAGAG GCCTGAGAGC 50
AGGAGGCGGAA TTCGATCTCT CCTCACAAAC AGCCCAGGAA AATATACACC 100
40 CCGGGGGGAAG CC 112

55

(2) INFORMATION FOR SEQ ID :70:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :70:

AAGGGTCTCC AATTTAATCC TTGGGTTGTT TTACCACTTC TTTCGTAAAT 50
15 TTATCAAGAT TTCTTTTCGCA CAAATACTCT AGCGCCTCAC AACAAACCTG 100
ACCTTGCGCA GGAAGTCGAC CATCAGCACC CCCTTTACAA CATCGTTCAT 150
ATCACAATTG AGAAGATGAT GAATGAAGAT TCGCTTCCAA GTTCCAAGGG 200
20 CAGATTTATT CCTTTAACTG ACATTTCCAT GA 232

(2) INFORMATION FOR SEQ ID :71:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :71:

35 CNTGGATCCG NCCTTGTTAC GNCCAGGACG NCTGGACCGC AAAATGAATT 50
TTCACTTTTTC GACCACCGCC AGAAGAGATG ATTTTCTCAT CATNAACAAG 100
GAACCTTTGA GGAGATCGAC TGAAAGACTA GCGNCCCNGT CAGATAAGAT 150
40 TTAGGGCTGA 160

(2) INFORMATION FOR SEQ ID :72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :72:

AAGGAAGACT GGTTCGCCAT CCGAGATCAT TAAAAANGNC TGACCCTAAC 50
AATACGTACA AAAATATATAA ACGCAAATAA AAAATACAAA CAGATTCTT 100
CTTAAAGTAC TTTTAAGAAA AAAAGCAGGN CCTTGAAGT TTCGATTCTT 150
TTTCCTCCC GTCGCAAATT CTATGTTTGG AT 182

20

(2) INFORMATION FOR SEQ ID :73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :73:

CAAGAGGCAG CTGCCCCCTCC CACCTCGGAG GNCTGAGAGG GNCTGTGNCG 50
ATGAGCTGGA CGAGCACAGC ACTAAAAAGG CTTGCCCTNG CACAATAACA 100
CTGAGAGGAT GATGAGAACA CNCTTGAAAT GCTTCATNCA CATGGGCAGG 150
ANAGGCTGCA CAATGAAA 168

40

(2) INFORMATION FOR SEQ ID :74:

57

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :74:

10

AACCTTTATT CATCCTCTCN TCCAAGACCT ATGAGAAGGT TCCAGGCCCC 50

AGGAACACAG GCTTCTTGGC CCCAGATGCA CCTCCCTGCA CCCCAGGGGT 100

15

GTATACCACA CCCCAGGGCCC CTAATCCCAG GCCCCGAGAT AGGAAAGCCA 150

ACTAGTTCTT TNTNTGTGAT TCAGTAGGCC TGACCTATAG NTGGAATGTC 200

NCTNTCCCTN NAATAAATTN C 221

20

(2) INFORMATION FOR SEQ ID :75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :75:

AGACTGNTTG GGTCAATCCGA GATCATTAAA AATGNCTGAC CCTAACAATA 50

35

GGCACAAAAA TAAAAACGAA ATAAAAAACC TCCTTANNTT CGAAGTATCT 100

TAGAAAAAAA CAGGGCCTTG AGTTCTG 127

(2) INFORMATION FOR SEQ ID :76:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs

58

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :76:

AAAAGAACAG CAGTTTCACA TTTCACATAT TTGAAAAACA TTTCAAAACC 50
CTCTAATAAG TATTTAATGA AAATAAATTT ATCGAAGAGA AACAAATGACC 100
ACAAAATTAA TACTACCAAA TCATTACTGA GACTCTTGCA TTACAATATT 150
TGGAGAGTAG GTGAAGAAAA TNTAGACCGA 180

(2) INFORMATION FOR SEQ ID :77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :77:

GATTAANNNN NNNGCACCCN NNATTACTGG CACAGCTGGT GAATATTTTC 50
GTGGACTTTT GACTAGTGCA CCTGCGTGCG GGAAAACANT GATAAACTG 100
TCACTTTAGC CNCNAACTAC AAGACCNGTT AGACTAGAGA GC 142

(2) INFORMATION FOR SEQ ID :78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :78:

GGCCCTGAGA GCAGGACGGC GAATTCGATC TCCTCCTTCA CAAACAGCCC 50
5
ANGGAAANTA CACCCCGGGG AANNCCCCNC NCNNTTAGAA CCNNCAGGNT 100
CTGNCCCCCC CNNNGNCCCC CCG 124

10 (2) INFORMATION FOR SEQ ID :79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :79:

AGGTATAGTG TTCCCTAATC ATGTACTTGT GAAGCACCCG GANTTTTTCA 50
TATAGTCTAA AAGCTAGAAG AACAAGAGTG TATTTTCGTGG GTGGATGTAT 100
25 NGTCACTTGC TGAANNNTT GAAATACCAT TATCCCCCTT GCTAACNCCT 150
TTAAGNAAAN GCCNTTTTAA G 171

30 (2) INFORMATION FOR SEQ ID :80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :80:

CTGAACAGTG TGGTCGAGCA TTCCAAGTCC GTGAAGGTGC AGGAGCGGTA 50

60

CGACAGTGCC GTGNGGGCAT CATGGCACCT NGACCACGGG CNCCTAAG

98

(2) INFORMATION FOR SEQ ID :81:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :81:

15 CCTCAACAAG TCGAGACCT GGGCGTCCAA CTGCCTACA ACCACAGCCG 50

CGAAAGAAGA AGACCTGCTG CTTCAATACA ACACGGGAGG ACCTGGCCAT 100

CAACATCA 108

20

(2) INFORMATION FOR SEQ ID :82:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :82:

ACACATNACC CACNGCCAGT ATATCTCGAA CAAAGTCTCA GACGATACTC 50

35 CCTAAATTG TAAAGCTTAA TACAGGTTNT GGAAATCATT TAACACCCGA 100

GAATGTCCCA TCACAGTCTT CCGTCAAAT TTAGCCTCAC AACAACAACA 150

ACGCCTACGA AATTCTAAAT TCAGAAGGAA 180

40

(2) INFORMATION FOR SEQ ID :83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :83:

10

GGCTTCTGAT CGCCATCCTT GAACAGGGCA AAGGTGGCCT CACCAGCCTT 50
CGATGCAGCT GCCATGCGCG CCAGAATCAG CGAAGGCATA CCCTTACGTC 100
GTTGGACGCA TGTTTAGATG CCTTTGAGAC CGCCCAGAGA AGTCCTTGTC 150
CTTCTTAATA AACACCTCCT CGCCAACTGC GACGACCACA ATCACCGTA 199

15

(2) INFORMATION FOR SEQ ID :84:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :84:

30

CTTCGGTAGT GCCGCCGTGG TGCCACACAC CGTTGAGGTT GGAGTGGGCA 50
CAGGCATGGT ACCACCAGCC TCCCCGCTGG TACAGGGCAC AGTTACCTGA 100
GGGGAGAGAG AGAGTCCATG TCCTCTCACC AGAATAAAAG CCTCTACCTG 150
CACCTCACAG TGCAAGGCTT TTGCCAGGCA TCCCCTGGCC CCTCCCATT 200
NACNGAATAC AACC 214

40

(2) INFORMATION FOR SEQ ID :85:

62

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: r. leic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :85:

10

CCTGGGCAAG CTGAATGTGA AGTTGACCAG GCTAACTGAG AAGCAAGCCC 50

AGTACCTGGG CATGTCCTGT GATGGCCCCT 80

15

(2) INFORMATION FOR SEQ ID :86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :86:

GGGGATAGCT GGCTCATCCT CGGAAAACAG ACCCACATCT CTATTCTTGC 50

CCTGAAATAC GCGCTTTTCA CTTGCGTGCT CAGAGCTGCC GTCTGAAGGT 100

30

CCACACGGCA TTGACGGGAC ACAGAAATGT GACTGTTACC GGATAACACT 150

GATTAGTCAG TTTTCATTTA TAAAAAAGCA TGACAGTTTA TTA CTCTGTT 200

35

TCTTTTAATG 210

(2) INFORMATION FOR SEQ ID :87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :87:

CACAAAAAGC ATGATCAGGG CTAGCCTCAA TACAGGGAGA AATCATGGAT 50
ATTTAAAAAT ACTTTTTTTG ATTCAGATTC CGGTATGACT GAAGANGCAA 100
CA 102

(2) INFORMATION FOR SEQ ID :88:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :88:

25 GATAGGCGCA TGCATACTAC GGCTAAGGAG AAACAATGTT CCTACATATT 50
ACGGGCAGTG AGAACATTAT CTGTATAACA GGAAGTGTGA TTATTTAAAA 100
ATAGCAGAAC TTATCNGTCT GTGCTTTAGA AATAACTGTA TACAGTGTTA 150
30 TAAGTTGAAA AGAACTCAAA ATAATAATA CAAATAAGAA CCTACGTATT 200
AGAATTCAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA 250
35 TGACACAAAT TCAAAACACG ATCAT 275

(2) INFORMATION FOR SEQ ID :89:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :89:

GCCTGATGGT ATATACTGTT TTGCAATTGC ATACAACTGT GCATTACAAA 50
TTAATAGTAA TTATGGTTTG GNNGTAAAAT CGAGTTTCAG AATAAAATNA 100
10 AAAACAATAA AATCCAAAGA ACGATGTAAA CAAAAAGCT TTTGTTTTGT 150
TACAAAGTAT ATTAAGGATT TTCTGCTAAG ATTCAGTTTA AGAGTTTTC 200
15 TCGTGAAAAC TAAGTAGAAA CACAATGCCA ACAGCTGGCC AGTAATCAGT 250
GCTGTGTACT CCA 263

20 (2) INFORMATION FOR SEQ ID :90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :90:

30 GCGTCCTGCC CAACATCCAG GCCGTACTGC TGCCCAAGAA GACGGAGAGC 50
CACCACAAGG CCAAGGGCAA GTGAGGCCGC CCGCCGCCCC CGAGGGACCC 100
35 CTTTGAGA 108

(2) INFORMATION FOR SEQ ID :91:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

65

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :91:

	GCCTTGGTGG AGGGCATGAG GCTATGATGA CTATTGGCTA TAATATGGAT	50
	ATGGCTTTGG CTGATAGATT TGAAGAGACC TCAATTACGT TTTTCAGGAA	100
10	TGTTTGATCA TAGATACAGA GATGGTGGTC CAGTTTTCAG AGCACCACAG	150
	GGCACTGTGT ACACATGAGG GGTTACCTTA CAGAGCCACT GAGAATATAT	200
15	TAATAA	206

(2) INFORMATION FOR SEQ ID :92:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 210 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :92:

	CCTTGGTGGA GGGCATGAGG CTATGATGAC TATTGGCTAT AATATGGATA	50
30	TGGCTTTGGC TGATAGATTT GAAGAGACCT CAATTACGTT TTTTCAGGAAT	100
	GTTTGATCAT AGATACAGAG ATGGTGGTCC AGTTTTCAGA GCACCACAGG	150
35	GCACTGTGTA CACATGAGGG GTTACCTTAC AGAGCCACTG AGAATATATT	200
	AATAAANNNG	210

(2) INFORMATION FOR SEQ ID :93:

40

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 189 base pairs

66

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :93:

AGGACTTCAT CCCAGACTCA CTTGTTCTGT TACAGAACT AACCTAAAAG 50
10 GCTGGAAATT AAAGGATACA ACCTAAGAGG TTATAACAGC AGACTGGTAA 100
AACATGGCGA AAGGAGCTCT CTCTTTCCCC GCAGTCTACC AAGCTCCTGT 150
15 GCATTTTCAC CACATAGATC TGCTAGCTTA CAAATGATG 189

(2) INFORMATION FOR SEQ ID :94:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :94:

GAAGTGACAG GNAAGCTACA GGTGTATAAC AAATTTGTAA ACTAACCAAG 50
30 CACAATGTGG CAGGGCCTAG CTGCTACAAA GAAGACAATT TAACAAATAC 100
TCAACGCATG ACAAAAAACT CAGGACTGCA TTTGCACTAA TCGATAACGN 150
35 GTCATTTAAT 160

(2) INFORMATION FOR SEQ ID :95:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

67

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :95:

TGCTTTATAC ATNATNAAAG GTAGGCACTT CATAAAATTT GCATTTTGGT 50
AAAAGGCAAC AATTTGATGT CAGTATCTTA ATTGTGTCAT TAACTTTTTT 100
10 AAGAGAACAG ATTATCAAAA TTTTACGAAG AAGAAAAAAA NTATAGTTTT 150
TAAGGAAACT ACAGAAGGGA T 171

15 (2) INFORMATION FOR SEQ ID :96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :96:

GTGGATAAGA AGATGTGTAC TTGGGAACAA GGCTAAAGCC ATTGGCTGAT 50
TTCCCCAACC TTTTATTCG CGAAGAACT CCAGTTGTTA ACTTTTTGAG 100
30 AGTTTTTTTT GGCAAAGAA CTNCATTAN C 131

(2) INFORMATION FOR SEQ ID :97:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :97:

5 GTCCTAATAT TTCTGTNCAG AAATTGTCAA CTTGACTTGA GAGTTGAGAA 50
GTAAAGTTAA GGCAGTGACA ATATATCAGA ATGGAAGTCC TTAAGAGCAA 100
CTAACAGGTT CTTGATCAGA CTGACTATCT TTTCTTAAGT TCATAATATN 150
TTACTGTCCA GCCAACTATA CTTGGATCAA AATATCCTTC ATGAAGGGCC 200
10 ATAATGTATT GATGATCTGC TGTAACCTTG AGAAGCTTCC TGAAGCTCNT 250
TTTGAATAAA TTTATNGAAC TTATGAAGA 279

15 (2) INFORMATION FOR SEQ ID :98:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :98:

GTGAGTCTTT CTTCAACTAG GGAATGTTT CCAGGGCAGC CCAGGCCTCA 50
CTCAGCAGG CCTCCGCGAC AACTGTTT CACTGACTGA GGATGAAGTG 100
30 AAATCCTGAA AGCTGAGAGC CAGCGCCCTC ACACGAGGGC TGGGACGTAA 150
CAAAAGCCCA TCAAGAGTTT TGCCCAGGGC TTTCTTGAGC CTTGAAGCAT 200
35 GACGAGACCA GGACCCTTA GGATTAAGCA AGTTTTATGC GGTCTNAAAA 250
AACTCCAGGG CCTCCA 266

40 (2) INFORMATION FOR SEQ ID :99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs

69

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :99:

GGGAACATTT ATTGACATGA AAAGGTGTTT CAGATATACT GATATGTCAA 50
10 ACAAATAGTA AAACAACATA GAGTAATGAT TCATTTTGGT AAAAAATATA 100
TATGTATATA TAGAAAAAAA TTCTGCAGGA CATATGCTAA ATTGGTAACA 150
15 GTGCTTACCC CTGGAAGGG GGTATACGAT GTTGATTAC TCTTTGGGTA 200
CGTATT 206

(2) INFORMATION FOR SEQ ID :100:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :100:

30

CGCAACTNTC NCTAAACATC CAGTTTTCTA ATNTAATAAA AAATGGCAGT 50
AATTATCCTC ACCTCTCAGG GAA 73

35

(2) INFORMATION FOR SEQ ID :101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :101:

5 GAGCACAATC ATGNGCAAGC GCAACAGCAC ACCTTTATCC GAGTGAGACC 50
ACTATGCAGC NGAACAGAGA CTTCTTATCT CTTCTTCTTG ATACTTGAAT 100
ACTGCCCC 108

10 (2) INFORMATION FOR SEQ ID :102:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :102:

GAATTATCAA ACCATCNTTG CTGACATTAA TTTCCAGCT TTGATCTTAN 50
NTCTNGCTTT AGTCCTCATA CAATGACTGT GTTTTTCTCA AACGATNTAT 100
25 CGTATAGGNA TCCTTCTAAG CAATCCTGCA CCCACAAAAA AGCTGCATCT 150
TCAATATAAC ANAAAAAGGN ATTTTGCAAA AAGTACAAGT TTTATGTCTN 200
30 CTGTTAACTG 210

(2) INFORMATION FOR SEQ ID :103:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :103:

71

CGTAGTTCGA TTCGAGTGGT CTATACAATC ACACCAAGCT TGATGTTGAT 50
 GTCACCAAAA TTTCTTTCCA AAAAAA 76.

5 (2) INFORMATION FOR SEQ ID :104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :104:

CTTATGATTA ACTAAGCAAA TCTTTCATAG AAAGATATTA TCAAAGCTGA 50
 AGAAATGCAA ACTTNAACAA AGTGCCGTGA GATTCCGGAA AAACCCTTAA 100
 20 CCGATTGAAT GGTTTTTTAA GAATAAAAAA GAAGTCTGAT ACTGAACTAC 150
 AAGTCGCAAG GAACATC 167

25 (2) INFORMATION FOR SEQ ID :105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :105:

TATCTGCATA TCTAAACATA GAAAAGCACA ATAAAAACAC ATATCATAAC 50
 CTCACGGGAC CACCATCATA CAGCAATTG TCATGATCAA AAGAAACATC 100
 40 ATTAGTCGTG CCATAACTGT AT 122

(2) INFORMATION FOR SEQ ID :106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :106:

GAATTCTTCA CTCCAGATTT CCAATGCCAA GATACATTGA TACTGAACAT 50
GGAGGCAACC AGGCCCGTTT CCTCCTTTCA AAGTCAACCC TCACAGACTC 100
ATAATAATAT GCATGCCTGG GGGCAGGAGT CTGGAGCACC TATTCTNACA 150
GATGATGTTA TTTACAAGTG TTTATGGATC ACTTGAAGAA ACTTGCTGTG 200
TCCAGTGCTG CTTGAAGTGC TAATAATGTT AAAGACACTT AAGAAGATGA 250
AATAA 255

25

(2) INFORMATION FOR SEQ ID :107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :107:

GGACGTGAAT TGGTGAATA TTTACAAAGA AACTGTTTT CTCAAAACAC 50
TGTTTCATTGG TTGCAAGAAT GAATACTGAC TTCAGAACTC AAACAATGGA 100
AGAACTTGCA TTTTATGGA ACTCAGTATT AAAAGAAAAT ATAATGTGAT 150

40

73

AGCACTTTGC AGATATGTCT AGACTGTGAT CTGAAGCATC GTAGTTTCCT 200
ATACCAAGAN ACANTTATGT GGTAAT 227

5 (2) INFORMATION FOR SEQ ID :108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :108:

GAAAAATNGC ATGAAAGAAG ACTCTNNNN NGCCATACCA TGGTACAATA 50
ATCATNAAAA NACAANAACA AAAACAAACA CATAAAACCA CTCACATATA 100
20 CATGTAGATA CAACAACNAT ATAATATCAA TAAAAAATAA ATAGNAAAAA 150
AAAAAAATAA CA 162

25 (2) INFORMATION FOR SEQ ID :109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :109:

AATTAAAAAT ATTAAACAAA ACTACCACTC CTCCTTATTA AAGCCCATAA 50
AAATAAAAAA CGAAACCCGA GAACCAAAAT GAACGAAAAT CTTTCGCTTC 100
40 ATTCATCGTC CCCACAATNC CAGGCCTACC CCCCACTG ATCATTATT 150

GTTT

154

(2) INFORMATION FOR SEQ ID :110:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :110:

15	ATGTGCCAAG TAAAAAATCA ATTNNGTNGCC TTTTTCATT NCGCGGACAC	50
	CCATAGGCAC CAAAAAAGG TGCTAATAAG TAACATGTTT TAAGATGCAG	100
	AATAAGCTAT GGAAACAAGG AATGCTCCAA GTGTCCCAGT CTTTCTCCTT	150
20	GCACTCCTTG TTAATAACAA TACACTATAT CA	182

(2) INFORMATION FOR SEQ ID :111:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 94 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :111:

35	GAAGGTGAGA ATAGGGTAGG GGAAACAGTA GGACAGGAAG TATTCACGTA	50
	CNTCAAAACC AATGGTAGAA CATCACATTT CAAACTGCAA ACCA	94

(2) INFORMATION FOR SEQ ID :112:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 92 base pairs

75

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :112:

10	TAGGGCAGTG AAACCTAATC TGCCTGATGC TATAANTGAN TGAATTACAT	50
10	GNTCATTNGT TAAATTTTGT TCTAAACCCA TTAGGAAATT GT	92

(2) INFORMATION FOR SEQ ID :113:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :113:

25	GATTGTTTTT GCATTGCGTG TGTCACACAG CAGCACAAAG ACAATATATG	50
25	TAAGCGTNNA TACACCAGAT TTGACACAAG AGATAGCGAA CACCACAAAG	100
30	ATTAGGACAG ACCGCGTATA GTAGCTCTGA GGA ACTCCAA GAATCTAGAG	150
30	GG	152

(2) INFORMATION FOR SEQ ID :114:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

76

(xi) SEQUENCE DESCRIPTION: SEQ ID :114:

TTGGCACTGA CATCCAGGAC AACAAATGCA GCTGGCTGGT GGTTCAGTG 50
5 TCTGCAACGG GCCACTCCAG AACAGTACCA ATCCTGAAGG AAAATACNTG 100
GCAGAAGGAG GCTGAGAAAG TGGCTCCGTG AAGGCNCTAT AGAGGGCTGA 150
TCTGCCAGCA TGTCTTCAAT ATGAGGAAGG CA 182
10

(2) INFORMATION FOR SEQ ID :115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :115:

GGCACTGACA TCCAGGACAA CAAATGCAGC TGGCTGGTGG TTTCAGTGTC 50
25 TGCAACGGGC CACTCCAGAA CAGTACCAAT CCTGAAGGAA AATACNTGGC 100
AGAAGGAGGC TGAGAAAGTG GCTCCGTGAA GGCNCTATAG AGGGCTGATC 150
TGCCAGCATG TCTTCAATAT GAGGAAGGCA NT 182
30

(2) INFORMATION FOR SEQ ID :116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :116:

77

GAGGTTCTTG AATATGTATT TTTTACTGAA AAAATCATTC ATAAANTAAC 50
ATACAAAAT GTACAAACAC ATGAGTAAAT AATGTAATGA CAAAGGACTA 100
5 TTTTCGGAAA AGTGTTTTTT AAAACANNCT AGATTTCAGT GCAAAAATGT 150
ACCCCTGGCA CCTCTTAAAA CGTAAGAGCA AGCTCAAAA CACGTAGTGA 200
TGGAATAAG CTAGCTACGC TCAATGC 227

10

(2) INFORMATION FOR SEQ ID :117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :117:

CGAGAGATTG GTAATGAGGA AGCAATTTGG AGGGGNGGAA GCTACAANGA 50
25 NNNNGGGAAT TACAACAATC AGTCTTCAA TTTTGGACCC ATGAAGGGAG 100
GAAATTTTGG AGGCAGAAGC TCTGGCCCCT ATGGCGGTGG AGGCCAATAC 150
TTGCAAAACC ACGAAACCAG GT 172

30

(2) INFORMATION FOR SEQ ID :118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :118:

78

50
AATGATGGAA GCAATTTTGG AGGTGGTGGG AGCTACAATG ATTTTGGGAAT
100
TACAACAATA GTCTTCAAAT NNGGACCCAT GAAGGGAGGA AATTTTGGAG
150
5 GCAGAAGCTC TGCCCCCTATG NCGTGGAGGC CAATACTTTG CAAAACCACG
200
AAACCAAGGT GGCTATGGCG GTTCCAGCAG CAGCAGTAGC TATGGCAGTG
210
GCAGAAGATT

10

(2) INFORMATION FOR SEQ ID :119:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :119:

50
GGTAAACACA AAGAGTTTCT GATAGTGTCT GCACAACAGC AAACCAACAT
95
25 TTGGTGAGGA ATTAGCAATT TCTTGCCAAA GAAAATTGAT TCTGC

(2) INFORMATION FOR SEQ ID :120:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :120:

50
GGAGTATTTN AANNTTTCOA ACTTTATTAC TTAATGAAAC AGTTTCTATA
100
40 TACTGCTTCC AATATACTTT AATCCTTTTT TTCTCGTTAA ATTTTTTTTTG

79

TTGTTCTTCA GTTGAGCTGA GATACTTTTA ATTACTTTTT ATTAAGTCT 150
TCCAGAAACC GTAACAGG 168

5 (2) INFORMATION FOR SEQ ID :121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :121:

GGAGTATTTA TCTTTCAAAC TCCNACTNA GTGAAACAGT TTCTATACCA 50
CTGCTTCCAA TTACTANCTN TTTTNTCNGT TAAATTTTCN NCTGTTTTTC 100
20 AGTTGAGCTG AGATACTTTT AATATNNNGT NACTGCTTCC AGAAACCGTA 150
ACAGGTGCAG GAATAATTGA TGATATCCAA GTAGAGGCTG ATGNCAGCTA 200
25 ATACATACTT CGGTGACNTT ATGCATCATG A 231

(2) INFORMATION FOR SEQ ID :122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :122:

TCTATGGCAT GAATGTTTGC AACCAACNNN NNGGAAAGCC TTAAAGGAAT 50
40 AGCTGTTTAC ATAGGAGACC GTGACAATGC TGTACGCAAT GCTGCACTAG 100

82

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :127:

TTTAGTTTAC TTCTGTTCCA CCTTTTATTG AAATATTAGT TGTTAGGCTG	50
10 AAAGCCTCCA GTTAAGAACT TGCTGAGTTT TTTTGTTTCAG CAACTTGACA	100
TTTACTATGC GCATTATATA NCTCAATTAT GTCTGTTTTT TATGCTAAGT	150
15 AGGAAAACCA	160

(2) INFORMATION FOR SEQ ID :128:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 150 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :128:

GCCCACAACT TACATCCTCA TTATTGGCGC CTACAACTC AACTACGAAC	50
30 ACACTCACAG TCGCATCATA ATCTTTTGAG GACTTCAAAC TTACTCGGCT	100
ACCGCTTTTT GATGACTTCT AGCAAGCCTC GCTAACCTCC CTTACCCCCC	150

35

(2) INFORMATION FOR SEQ ID :129:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 182 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :129:

5 AGAGAGACAG ACACCATGGA GCCACAGGGG CAAGAGGNNG NTTTCCGAAG 50
CAGGGGANNG GCTATCACTC GGACGGACCN NNGCTCAACG AGTCCCACGA 100
GAACACACCA GAAATTTGTC ATTGCACTCA ACCAAAATCG ATATCAGCAA 150
10 TGAAAAACCC AAAACAGTTA CGANGCTAAT CC 182

(2) INFORMATION FOR SEQ ID :130:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID :130:

GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT 50
25 TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGTC 100
TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT 150
30 TCAACCAAAA TCGATATCAG CAATGTAAAA ATCCCAAAAC ATNTTACCGA 200
TGCTTACTTC AAGAAGAAG 219

(2) INFORMATION FOR SEQ ID :131:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :131:

5 AATAATTCAT CCACTTATGG AGGAGGAGGA GAATGTGGAA GAGGTAAAAA 50
GCTGGGCACA AGTTCATATG CCTATGAGTC AGTAAAGACT GAAGTAATGT. 100
CCTATGTTGA GCTGGTTATT TTGATATATG ATAATAATTA TCTTTGTAGT 150
AGAACATCGT TAACGGAATC ACAGATATAT C 181

10

(2) INFORMATION FOR SEQ ID :132:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :132:

GACCAGCAGC TGTGGACATT ATGAGAAAGT GAAACCTGAG ATCCNCTGTT 50
25 GATTGAGAAA TGCAACACCT CAAAATGNGG GACAGCTCCT GATTACCAGG 100
TAGAAGATGN AAACAACTGG GGTGTCCATT CAGGAGGAAA CAATTGCAAG 150
CTAAGAACTG TTGAGAGTGA AGCTGCATTT TCTGNACC 188

30

(2) INFORMATION FOR SEQ ID :133:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 190 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :133:

85

GAGGTTGGGT CGTTGCATCC ATCATCAGGA GTTGACTTGT TCTGAGCAAC 50
TGAACAGAAC ACACCGCGAT GCTCTCGACA CTCCGCTCCT GGA CTTCAGT 100
5 CACGAGTGAG TTGATGGTGA CTTGACCTGA GAGATTTTAC AGAAGCTCTG 150
TGA CTTGTT GTGGAAGAAA TCTGAACTGT TCAAGTTAAC 190

(2) INFORMATION FOR SEQ ID :134:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :134:

20

ACATTACGAT CACTGATAGT TGGTGTGCGA CTGAAACCCA CATTNTGGTC 50
AATCTCCTCG TAGAGCTTCT TCTTCACCTG AGGATTGGCA GCAGGAAGGC 100
25 CAGGGTCCAT TTA ACTAAGA GGTGGTGATC TCCACGCCAG CCCCAAAGAT 150
GTCCCCTATA TGGTGAGAAT GNGTCATCTG AAAGCAGCTC TGAGTCTTGA 200
TCTGGGCCAG CATTGCCATT ATTGAGTTTA TCTAG 235

30

(2) INFORMATION FOR SEQ ID :135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :135:

86

GAGAAACAGT ACCATCCANG ACACGATGTG GTGGAGGTTG ACNCCGCTGT 50
ACCCCAGAGG AGCNCCACCT GTCCAAGATG CAGCAGAACA CTACAAAATC 100
5 AACTATGTTT TTTAGCAGAT GCAGGACTAG ACCCCCACGC AGCTCTG 147

(2) INFORMATION FOR SEQ ID :136:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :136:

GAAAAATGNG TTGANCCATT CATCCACAAA TTGACTTGCC TGAACAACCA 50
20 CCAAACAATA CACTAATGNT TCACACNTTT NCTTTTACTT GNACNTTAAG 100
NTCCCAANTGA GTCACGGTGA CTTACCCTAA ACATCTCAAN NGTNNTCTGA 150
25 CTNAGAATGC GGAGGAGATC T 171

(2) INFORMATION FOR SEQ ID :137:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :137:

ACATATATGT GGTAGGATAG AGAGATGGNN NNNGTGTATG ACATAGGTGT 50
40 TTCTCGTGTG ATGAGGGTTT ATGTGTTATG TGGGGTGAGT GAGCCCATTG 100

87

TGTTGTGGTA ATATGTGAGG AGTATAGGCT GTGACTAGTA TGTTGAGTCT 150

GTAAGTAGG 159

5 (2) INFORMATION FOR SEQ ID :138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :138:

CCCACGACTT ACATCCTATN ACNCTTCGCC TAGCAAATA AACTACGAC 50

NCACTCACAA TCGCTCATAA TCTCTTNAGG ACTTCAAAT NTCTCTNTGA 100

20 NCCTTTTGAT GACTTCTACA AGCCTCGCTA CCTCGCCTTA CCCNTGTNC 150

TNCGGGAGAA CTCTCTGTGC TGTACCACT 179

25 (2) INFORMATION FOR SEQ ID :139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :139:

GACCTGGGAC GTAAATGATG AGACGGGTAC TTTGGCGGAC ATGAAGGAAC 50

TGGCATATGG AACCTTGGCT GTGAAGCTGC AGACTATAAG ACAGCATGAG 100

40 ACGACAATTC TGCTACTGCA ATGATGACAT CGTTTCAGAC CACAAAAAGA 150

88

AAGGCGATGA CCAGAGCCGC AAGGCNG

177

(2) INFORMATION FOR SEQ ID :140:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :140:

15 GTTTACAACA TTTACATCCT ATGAACTCAT GGATTATAAA ACATTTGTGA 50

CTTATACTGT CTNTGTCAGT TA 72

(2) INFORMATION FOR SEQ ID :141:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :141:

30

GTNGGCTGAA ATGAAANAAT AAAACCAAGA AACGAATTTA AGTATTNGTT 50

TTAGTACGNA AA 62

35 (2) INFORMATION FOR SEQ ID :142:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :142:

5 ACCAGTNNNT GATTGGTAAA TGGGAAATAT AATTGATTCT GATCACTCTT 50
GGTCAGCTTC TCTTTCTTTA TCTTTCTTTC TCCTTTTTTA AGAAAACGAG 100
TTAAGTTTAA CAGTTTGTGA TTACAGG 127

10 (2) INFORMATION FOR SEQ ID :143:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :143:

AATATAAAAG ACAGCAGTTT CACATTTTAC ATATTTGAAA AACATTTCAA 50
AACCCTCTAA TAAGTATTTA ATGAAAATAA ATTTATCGAA GAGAAACAAT 100
25 GACCACAAAA TTAATACTAC CAAATCATTA CTGAGACTTT TTGCATTACA 150
ATATTTGGAG AGTAGGTGAA GAAAATATAG AACAGAACAT GNACATTT 198

30 (2) INFORMATION FOR SEQ ID :144:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :144:

GTTTCTCTNT ACGTCATCCA CCTTGACATG ATGGGTCAGA AACAAATGGA 50

90

AATCCAGAGN CAAGTCCTCC AGGGTTGCAC CAGGGNNTAC CTAAAGCTTG 100
TTGCCTTTTC TTGTGCTGTT TATGCGTGTA GAGCACTCAA GAAAGTTCTG 150
5 AAACTGCTTT GTATCTGCTT TGNA 174

(2) INFORMATION FOR SEQ ID :145:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :145:

GAGAAATAGT ACTTTAAAT AAAACTAACA TGGTTTGATC AGCTTGAAAT 50
20 AAGATTCATA AAATGTACCT TTTTGTATTG TTTTGTTCN GAGTTTTCGA 100
TTGAGANCAT TTGGTAAAGA TAAAGAGGTT TCCTGGGTGG CAAAAAATTA 150
25 TTTTGG 156

(2) INFORMATION FOR SEQ ID :146:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 35

(xi) SEQUENCE DESCRIPTION: SEQ ID :146:

AAGATTCNNN NNTCCATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG 50
40 GTTGGAATT GGCTGTTTTG TTAAATATA TCTTTTAGTG TGCTTTAAAG 100

91

TAGATAGTAT ACTTTACATT TATAAAAAAA ATCAAATTTT GTTCTTTAAT 150

T 151

5 (2) INFORMATION FOR SEQ ID :147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :147:

CTTTATTTTT CTTATACAGA TTCAGAGAAG TAAAANNCAG TACCAAACTC 50

CAGGTAANNT GGTTCGATCT GATCGATTG GCTGCATACT TTCGGTACGT 100

20 ATAACATTCT AAACCTAAAA TAGAAATTTT TATATTACAA AACGAGGAAG 150

TAAAATTTTA AAAGTTAAAG TACTAGC 177

25 (2) INFORMATION FOR SEQ ID :148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :148:

GATTCNNNNN TCCATTGAAT GTTACCTGTG CCAGAATTAG AAAAGGGGGT 50

TGGAAATTGG CTGTTTTGTT AAAATATATC TTTTAGTGTG CTTTAAAGTA 100

40 GATAGTATAC TTTACATTTA TAAAAAAAT CAAATTTTGT TCTTTAAT 148

(2) INFORMATION FOR SEQ ID :149:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :149:

AGATTCNNNN NTGGNATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG 50
15 GTTGGAATT GGCTGTTTTG TTAAATATA TCTTTTAGTG TGCTTTAAAG 100
TAGATAGTAT ACTTTACATT TATAAAAAAA ATCAAATTTT GTTCTTTATT 150
TTGTGTGTGC CTGTGATGTT TTTCTAGAGT GAATTATAGT ATTGACGTGA 200
20 ATCC 204

(2) INFORMATION FOR SEQ ID :150:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :150:

35 AACATCGAGG TCGTAAACCC TATTGTTGAT ATGGATCTCT ATGAATAGGA 50
TTGCGCTGTT ATCTCTAGGG AACCTCACCG TTGGCAAGTT ATT 93

(2) INFORMATION FOR SEQ ID :151:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs

93

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :151:

10	AATCGAGAGA AAAAATGATG ACACTGTAGC AATATCGTCG GANTCCACCT	50
	ACTTTGGGAT CAGCCTATCC ATCCGTGTCT TCCTATTTAA ATCGTCTATC	100
	CTCTATCCTT CCCCTGTCTT TTTNTGAAAA GGAAAAAAC CAGGAAGGTG	150
15	T	151

(2) INFORMATION FOR SEQ ID :152:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 109 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :152:

30	TCTGAGAGGA ATACTNNTAA GTGCAATGAA TATTGCAAAT TTTCCCCCCT	50
	CTAAGTAATT CCCGATATTA GCAAANCANN NANATTAATG TCCCAGTGAA	100
	TGTAGCCTC	109

35 (2) INFORMATION FOR SEQ ID :153:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 136 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :153:

5 AAAATTATTT TCACAGTCCC CCCCAACTCT CATTGCGTCG TTAAAGTCCC 50
TCCAATCCTT TTTTAGTTGT GAAAAAATAA GGGGCCTTTA AAGGAGGAGG 100
AGGAAAAGGG GAAAAAACC CATAATGGGC CTAAAA 136

10 (2) INFORMATION FOR SEQ ID :154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :154:

CATCTTCATC ACCATCACAA TACTCATCAT CACCACCCTT CATNCACTAT 50
CATCTTCTAT GACTGCAAAC TTCTTATCTT TCTCTTCATT ATAGAAAGTT 100
25 TCAAGATGAG TATACGCATC TATCATTCGA ATTGTGTCAT TAATTTGTAG 150
GGCCTCATTG 160

30 (2) INFORMATION FOR SEQ ID :155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :155:

ACCAGTNNNN NNNGGTCAAA TAGGGAAATA TAATTCGATC TCTCGAATCA 50

95

ACTCTCTGGG TCAGCTTTCT NCTTNTCTTC TATCTTTNCT TNTCTCCTTT 100
TTTTAAGAAA AACGAGTTAA GTCTTAACAG TTCTCGCATT ACAGGCTTGT 150
5 GACTTCATGC TTAGTGTAAG GTGGAAGTTG AGATATTTTA A 191

(2) INFORMATION FOR SEQ ID :156:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :156:

CAACTGAACG CTTTGGTCAG GCTGCTACAA TGGAAGGAAT TGNGGGCNAN 50
20 TTGGTGGAAAC TCCTCCTGCN NTCAACCGTG CAGCTCCTGG AGCTGAATTT 100
GCCCCAAACA AACGTCGCCG ATACTAATAA GTTGCACTG 139

25 (2) INFORMATION FOR SEQ ID :157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :157:

GGTACAGAGC ACTCTGTACC AACACACAGA ATTTACTGTT CTGCAAATGA 50
CCAATACTAA AAATTTATAA AGATGTGCAC AATTNNNNGC AGGCAATCTT 100
40 TCTTTTGTTT ACAAGATACA ACATTTAACA GTTATTAAAT GTAATCCTGA 150

AGCACCCGCA AATTACCTT TG

172

(2) INFORMATION FOR SEQ ID :158:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :158:

15 GGGTGGCTGT TNNGTATATC TCGTTAGTAA ATGTACATGC TCTTCAGGTT 50
CTAGGGCTCC TGTTAGGGGA GGGAGAAATG TTGAAGNNGG GGG 93

(2) INFORMATION FOR SEQ ID :159:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :159:

30

GNATTTTTTT ATTGATATAT CATAGTTGTA CAAACATTTG GGAGTNCANG 50
TNGATACTTT GATACTATCG TGTNNNNNGG ATAATCACCA AATTGGATTC 100
CA 102

35

(2) INFORMATION FOR SEQ ID :160:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :160:

GCTTTTNNNN NNNNNNNNNC AGGTTTATAT TTACAATAAT TATCTTCCTA 50
TAGAAGCAAT AANNCNAGTA TTCTCCAGTA ACAACACANN NNNATATTCT 100
10 ACTCATCAGA GTTGGGAAAA ATAGGAATAA AGCAGATTCC ATACAGAAAT 150
ACCGTACTCT GCATATGTAC AAATAAATTC AATATATTAA ATCATTTTGA 200
15 GCGGA 205

(2) INFORMATION FOR SEQ ID :161:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :161:

AACTTTTTTA ATGGGTCTCA AAATCTCTGA GACAAAATTA CTNNGNNNAA 50
30 AGTTGTTTTTC CATATAAAAA ANNNNNNTGA TTTTAAAAA ACTAANNAAC 100
TTAAAAACNT GCCACACGCA AAAAAAGAAA CCAAAGTGG GNCACCAAAA 150

35 (2) INFORMATION FOR SEQ ID :162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :162:

5 TATTCAAAG AAAACATGG GTAAAAATGA TAGTGTTAA TCTGGCTCT 50
GTGTACATAG ATAGATACCT GTTACAG 77

(2) INFORMATION FOR SEQ ID :163:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :163:

20 GAAAATTATT TTCACATCCC CCCCAACTTC TTGCTCTTAA TCCTCATCTT 50
TTAGTTGAAG AATAAGGCTT AAGAGAGAGA AAGGAAAAC CATAATGGCT 100
AACTTAGCAG CACAACACGG TTCTTTTATC AAGGCGTNAT CATCATTTCT 150
25 CAAACTGACA TGCTACAGAA ATGTCTTCCA AA 182

(2) INFORMATION FOR SEQ ID :164:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :164:

40 GAGGGAGCAA AGAGAGCCAT AAAGGCTCGT GCTGGGAAAG AAAGCTGTTA 50
TGCTTAGACT TCTCTAGGTG AACTCAGAGT CTTCAAAGAG GAAATGTTAC 100

99

AAATTGTCAC CCGCCAGCTT TCTGGCCAGT AAGCAGAATG CCAGGTTGCT 150

CAGATTCACA GACATTTGCA AAACAGAAGA TG 182

5 (2) INFORMATION FOR SEQ ID :165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :165:

GTATCTCCCT CTACATCCCT CCCGAAATAC TAGGAATACT TATTCTATAT 50

GAGACATATA TACCACCCAA GTTTTAACAC CATATCCCAT CGGCTGTTAG 100

20 TGTATATAAA AAGAAATAA 119

(2) INFORMATION FOR SEQ ID :166:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :166:

35 GTACAAAGCC ACTCATCCTC GTGTGCCTAT CACGTTTTC AAACACATAG 50

GATCCCATCT CAGGAGCAGG ACCAGTGTTT AGCTAGATTA AACTTCGCTG 100

GTGATCTTGT TGATGCATAT AAAGTAATCT GGCATATATG GTTAAATTCA 150

40

AGATGTTATG GCAGAAGTGA CTTGTTTTGC TCAACAAGCA TTG 193

100

(2) INFORMATION FOR SEQ ID :167:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :167:

GTTCTGACTN AGAACTGAGC ACATAGCATT GACGCGGTAC CCTTGGAGAG 50
15 GGTGTGCTAG GAGGAGTGCT TGGCGAATTT GGACACGTAC TAATGTCTCT 100
GAGCCAGTCT GAATCTCTGT GAAGATGCCC CAGTGGAGGT GGCTGAAGAT 150
TAAATGGACA GTTTATAAAG TGTTCCTGGP GCCGA 185

20

(2) INFORMATION FOR SEQ ID :168:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :168:

GGACAACACA GCACCCATCC ACTACCCATT CAGAATTTAT ATAGAATATG 50
35 TACCCATGAT TATCTAGGTG AATCAATGCA ACAGTAGCTC TGATGTCCAG 100
ATTCCTAGT CTATTATTTT GTGTACAGAT CCTCTAACCA CTTAGAAATA 150
ATTTTAAATA ATA 163

40

(2) INFORMATION FOR SEQ ID :169:

101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :169:

10

AGACAAATTC NNNNTNNNNN NTGCCTGATA ATTCAGATG CCACCGTATA 50

GCAAAGGGTG AACATGTTTT CAACCCTTA ACTTTTACG GTGTTGAAG 100

15

ACCAGCTACT CCTTAATATT TATCAATGGA TTAAGAAGTT TAAGATTTTG 150

CAGATTTACA ATTTGGGTTT TTGTCTGGAG TTGCTTCGGT TTGAAGCCCC 200

CT 202

20

(2) INFORMATION FOR SEQ ID :170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :170:

TCAGGGAACC AAAAACTGG CTTGCTTGGC ACCCAGGGAC AGTAGCTGTT 50

35

TGGCTCTCCA CCCAATTAAA AAAACAAATC CCTGCCCTTT CCCCCACCCC 100

ACTAGCTAAG CAAGAGCAGA GCTCTGATGA AGAGCCAGTG CCGGGTGCCT 150

GGTGCCCAGG GCTGTAAA 168

40

(2) INFORMATION FOR SEQ ID :171:

102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :171:

10

AGAAGTCAAC TAAAGCTTCA ATGCATCAAT TTATAANGCC TCANAGATCA 50

GCAATTTATG ACACTTACAT TTACAGTCGA CCTTTACTAA CCAGGCAAAC 100

15

TTCCCGAAAT GATCAGGACT GATTCATCTC CTGAAATTNN CNGT 144

(2) INFORMATION FOR SEQ ID :172:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :172:

30

ACCCACAGNN NNNACCTAGA GGCCAGCGC CCAGAGAGGC ACGTAGAAAT 50

GGGGACAGCA CGTTTATAGA CCACCAGAAA TTGAAGAGGA A 91

(2) INFORMATION FOR SEQ ID :173:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

103

(xi) SEQUENCE DESCRIPTION: SEQ ID :173:

	GATTTTTTAA TGGGTNGCCT CTTTGTAGCTT GGAATATTAC GTTTACTTTA	50
5	ATCCAAGTCT AGGCCTTTTA AAGGGTCCTT AAAATTAAAG TTCAGAATGT	100
	GAATCCCTTT GACATCTATT ACAGGTTATA GGACCTTTTT GGTGTGATTA	150
	CGGTTTTCAA TACGATTGTA TAAATGAAGT TAACTTGGCA GAAGTTAAAA	200
10	TGGA	204

(2) INFORMATION FOR SEQ ID :174:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 241 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :174:

25	GTAAATTTC A CTACATCTTT TNNTNTGACT TTCATGCATT TCTCATACAT	50
	TNNTNNCNGA TGCTTGACTT TATTGCTTCC TAGCAATAAT CTGCATTTAA	100
	ACGAAAGGCG GTTCAATTCA TCAACTTGAA ATGACTATTT ATTTTNNAGG	150
30	ATTTTTTAGG GGAAGAGTAC CCATTTCGTT TATAAAAACA GATGACAAAT	200
	TTCTTAAAGA AACAGAAGCA CAATACTTTC GAAATACAAC G	241

(2) INFORMATION FOR SEQ ID :175:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 211 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :175:

5 GGTGGGCTCN NNNANNANNG TTCTACACTG TGGTATAAAC TTGTCGTGGT 50
TCTCGTGATA GAAACAGAC ACTGACCTTG GGTATAGTGG GCCTATAAAT 100
AACAAACCCT TGGGTACTCC TGAATAGGGG CAGGGCCCCC TGGGCCTCCC 150
10 TTACAGGTTT CTCAGGGAA ATGGTCCCTG GGATAATTCT TTAGGGCCCT 200
TTGGCCCTTT T 211

(2) INFORMATION FOR SEQ ID :176:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :176:

25

AAAATAAGAA TAAACATCCA TAATAGTNAT AGATANATCC NTTTATTTAG 50
NACATCAGCA ACGACTGCTT CACACCAAAT CCCTTCCTCT GNGAATGATN 100
30 TATATAACTC TAGTACTGCT TTCCATGAAG AACCTTGCAA ATTGATTGAA 150
AGTCCAGGAT NNCTCGCTAA TCCTCCACCA TAAGATTCT GACCTATGAT 200
AACTCCAAGG TGGCAAACAG AGAAATCAAC TTCCTTATAA ANAAATCCNA 250
35 AT 252

(2) INFORMATION FOR SEQ ID :177:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid

105

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :177:

	GCGGGCGACT TTCCATCCCT CGAACCAAGG CATGTTAGCA CTTGNCTCCA	50
10	GCATGTTGTC ACCATTCCAA CCAGAAATAG CACAAATGCT ACTGCGCGAG	100
	TTGCAGCCAA TCTTCTCAA GCAAACCGAC TTCCTAACAA CTNTCTACAT	150
	CTGGCTCGCT GCAGGCGACT CAATGAAATC CATCTTTAAC ACCACAATCA	200
15	TTGTTTNACA CCCAGTGTGC AAGCCAGGAG GGCATGTTCT GAGTCTNTCC	250
	ATCTGAAGAT ACCAGCTTCA AATACTAAT	279

20

(2) INFORMATION FOR SEQ ID :178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 base pairs

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :178:

	TATGCCCTGA AATGAAACCT CTAAGTTTGA CAAAATACCC AAAAAACAG	50
	ACCTTCCTNG TTAACACTTT ATAAGAAGGT GTGACATTTG GTGGGTGGTC	100
35	GTTCTCAATT TATAAANAA TAAATGACTT TAAAGGAGAA ATAAATTTAT	150
	GTCAGGA	157

40

(2) INFORMATION FOR SEQ ID :179:

(i) SEQUENCE CHARACTERISTICS:

106

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :179:

10 GATAATGCAA CTTTGTACAG GAAAGCGCGA TTTTACTAT

39

(2) INFORMATION FOR SEQ ID :180:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :180:

25 GCAAACCTCAA ACTACGGACG CACTCACAAT CGCTCATAAT CCTCTCTAAG 50

GACTTAACT CTACTACACT AATACTTTTT GATGACTTCT AACAAAGCCTC 100

GCTAACCTCC CTTACCCCCC ACTATTAACA CGGGAGAACT CTCTGTCTAG 150

30 TACCACA 157

(2) INFORMATION FOR SEQ ID :181:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :181:

107

CCATCCAGGC CAAATAAGCN CCGGCTATGC CCNTGTATTG GATTGCCACA 50
CGNCTCACAT TGCATGCAAT TTGCTGAGCT GAAGGAAAAG ATTGATCNCC 100
5 ATTCTGGTAA AACTGGAAG ATGACCCTAA ATTTTGAAGT TGATGATGTG 150
CCATGTGATA TGGTTCTGAC AAACCCATGT GCGTTGAGAG CTTTT 195

(2) INFORMATION FOR SEQ ID :182:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :182:

20

CATGGTCTTA ACCAGTGTC A GATGGAATCA GTGGATAAAT CCCCAGGTTT 50
GTTTGTCTT CAAATGGGAC AATTTGAGGA ATGCTTTAGG CAGAGGACTC 100
25 AGATGACAGA GCGCCAACCA CCCACAATAG AACCTGCTC ATCACA 146

(2) INFORMATION FOR SEQ ID :183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :183:

TAGAGGAATA GGGNNNGNGA CGCCCCNAGT TG TAGGGACG GACGGAGGAC 50
40

(2) INFORMATION FOR SEQ ID :184:

108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :184:

10

ACGNTTACGG TCACTGATAG TTGATGTGCN NCTGAAACCC ACATCCGATC 50
AATCTCCTCA TAGAGCTTCT TCTTCACCTG AGGATTGCGC AACAGGAAGG 100
CCAGGATCCA TTTACCACAG AGGCGGGATC TCCACGCCAA CCCCAGAT 150
GTCCCCTATG ACGACGAGAA TGTGATTATC TGAAAGCAAC TTGATCTTGA 200
TCTGGGCCAG CATGCCTCAT CTGATTCATC TCGCTTCCAT CAATGNGT 248

20

(2) INFORMATION FOR SEQ ID :185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :185:

AATGATGAGT AAAAGATTCA ACAACTCACA GCCCTGGGGG CACTCAGGCT 50
ACTGCTAAGG CCTGAGAGTT TTGCAAAAAT GCGCAGAGAA ACACCCTTTG 100
AACGTGGCTT TCT 113

35

40

(2) INFORMATION FOR SEQ ID :186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs

109

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :186:

10	GGGCCCCCTG ATCAATTCTT TGGATGCTTT TCAAATTTCC CAGGATCCCCG	50
	ATGTCGTCAT ACACTCCGAA CATGACCCTT TTTTCTTCCA ACGATCAACC	100
	ACTNCGNGGG ACGGGAGAGT GAGCCTTATA CCGATCAATC TGCACACC	148

15 (2) INFORMATION FOR SEQ ID :187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :187:

30	TCCTTACTGT AAGAGCCATT TAAACGATTA AAATCCCACT NGCCATACCG	50
	TAAGATGATA GGACCAACCA TACCTACCGA TCAAAAATTT ATCAATCCAA	100
	GCCAACTACA CTCCCACTGC TAAAAGATG AAAGGACCAA TCAAAGATTT	150
	AATTAACTA AAGGGAAAGA ATCAGAGACA GAGAATGAAG AAAGAAATTC	200
35	TAAGTTGCGA CGGACAAACC AGAACAGACA ATGAAGCCTT TCAACTGC	248

(2) INFORMATION FOR SEQ ID :188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

110

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :188:

TATGAAGAAG TGCAGCACTG GCCAACACCA GGGTTTACTG AATCATTTC A 50
GTTTAATACA TAAGTGTCCA ATAATAATGT CAACCCTCCC TCGCCACAGC 100
CAATAATTTG TCCTCACTGA GTTGGCAACA AGTGACTGCT GTGACT 146

(2) INFORMATION FOR SEQ ID :189:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :189:

25 ATTTACCACA AGGGACGATT TCCACACCAA CCCCCAAAAT GTCCCCTATG 50
ACGACGAAAT GTGTATTGTA AACAGCTCTG A 81

(2) INFORMATION FOR SEQ ID :190:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :190:

40

AAGTACAGCA TCCTGCTGCA AAAATGATTG TAATGNCTTC TCATATGCAA 50

111

GAGCAAGAAT TGAAGATGCA CAACTTCGT TCTGAATTG TGAGCTTCCT 100
GGATCAACTG AAGAACTTCT GAGGATTGAC CTGTCA 136

5 (2) INFORMATION FOR SEQ ID :191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :191:

AGGATTTAAG ATGGGGACAG ACTGGTGAAA ATGCGGCTGA CTGGAAGGAA 50
ATGGGGCATA CGAGTAATAT GTACATATCA AACAATCAAT TGCCTCCTGA 100
20 AATCAAAAAA TCAAATGGTG AAATGGAGCC TCCTTGATAG TTTAGGCCAA 150
CA 152

25 (2) INFORMATION FOR SEQ ID :192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :192:

TAAGCGAGGN NGTCTTTGAT TGCCTAGTAA GGTAAGACG ATTTTATAGA 50
ATNAAGGTGA TTCCT 65

40

(2) INFORMATION FOR SEQ ID :193:

112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :193:

10 AGGACCCAAA CTACCTTATT GCATTGAAG TTTTACTTAT NCTATTATAA 50
TCTAAGAGCC CACCCAACAA GGCACACAC ATAGATGCTC ACACTCTATA 100
15 GGCTGCCTGA TCCTGGACCA CCTGGGGCCC TGATTATGAT CTCCACGGGG 150
CTGTCAATGA CTAGGGAAAG CTTTTTAAGA CCCAGCGATC ATGCAATGGC 200
TCAACCATGG CGAATCAAAG TTAGCATAAT GTCCCAGCAA ACAATGTTA 249

20

(2) INFORMATION FOR SEQ ID :194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :194:

GGAAAGGGTG CCTCATCCCA GCAACCTATC CTTGTGGGNG ATGATCACTG 50
35 TGCTGCTTGC NNCTCATGGC AGAGCATTCA TGCCACGATT TAGGTGAATC 100
GCTGCATATG TGA CTGT CAT GAGATCCTAC TAGATGATCC TGACTAGAAT 150
GATAATTAAA AGTATTTACT TCGAAGCACC ATTTGAATGN TCAT 194

40

(2) INFORMATION FOR SEQ ID :195:

113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :195:

10

GTGATTTTAG TTTAAGGATA AGAAGCCACT ATATCAACGT CGGGGGGGTA 50
TTTAAGTCAC ACACATAGTT AACAAACNCNC GTNGCGTGCA ATAAATACCA 100
CATCCTTTNA TATGNNCNGN A 121

15

(2) INFORMATION FOR SEQ ID :196:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :196:

30

GGGCTTCNNN NNNNNNCATG TGCACTTAGA ACCGTTACTA ACCGAAACAC 50
CATTTGCTTG TCAACAATGT ACCCTTGACA GCAGGGAGAA ACTTCTTTAT 100
AGTCTCTGCT TCAGACAAGA TTTACNGCTT TCTCCAAGGC CAGAGGCAAA 150
TTGTGACCAC AAGTCTTGTT TCTTG 175

35

(2) INFORMATION FOR SEQ ID :197:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

114

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :197:

ACTGGCAACT TCTATGTACC TGCAGAACCC AAATTGACAT TTGTCATCAG 50
AATCAGAGGT ATCAATGAAA TGAGCCCCAA GGTTCGAAAG CTCGCAACTT 100
10 CTTACCTTC ATCAAATCTT CAACGACCTT CGCAACTCAA CAAGCTTCTT 150
ACAGTGAGGA TTGCAGAGCC TATATAGCTG ATACCCCAAT CTGAATCATA 200
15 AATGACTAAT CTACAAGCNT GTTATGCAAA ATAAATAAGA AACGACTTGC 250
TTACAGATGC NTTTAAATTG TGG 273

20 (2) INFORMATION FOR SEQ ID :198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :198:

GATTCCCCAA TAAGCAGACA CCTTGAACCA GCCTGGGGTG AGCGAAAGAT 50
GNTATA 56

35 (2) INFORMATION FOR SEQ ID :199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

115

(xi) SEQUENCE DESCRIPTION: SEQ ID :199:

5 GGACGCTGNN NNNNNNATCC TGCAATGCAC AGCACAGACC CCACCACAGG 50
GGTTTTATCC AGCCCAAATG TCAACAGTGT CAAGTTTAAG CAACTCTTAC 100
CGAGTGGGAC TCAATTCCCN AGTTGTATGG AA 132

10 (2) INFORMATION FOR SEQ ID :200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :200:

AAACTTTTTN GCACTTACAC AGACGAGACT TCACTGCNTG AGGATCATAC 50
GACATTTCAA TCGNACACAA ANTTAAAAAA TAAACAAAT TTTAAAAAAC 100
25 CATNTTGAAT TTCCTTAAAA TTATTCCAAT ACTTTCCAAC TTAAATTC A 150
GAACAAATCC TCCTAGAGAC TATCAATACC AATATCTTCA CATTGCTCAG 200
30 CTGNTACATA CGNCCCACCA GTTCACAACT AATGACACAA CACTACATGN 250
TCAAATCTTA TCTNNNATAG CACAGTAACA AAGT 284

(2) INFORMATION FOR SEQ ID :201:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

116

(xi) SEQUENCE DESCRIPTION: SEQ ID :201:

5 CCTGACACCA ATTTGCCCCA CATGTATGCG GGAAGAGGCC TGAGACTAGA 50
AGTCGTTGCC CTGTCCATCT CCCGGCCACA GGCTTCATTC CCAGATTTNT 100
CTTGNT 106

(2) INFORMATION FOR SEQ ID :202:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :202:

20

CTTTGGAAAA CAAACATTTN TTATTACTGA AATAGCAAAA ATCATTCTAC 50
ACTCCTCCTA AGCATGTTCA ATTAGCATAC ATTCCAACAA TGCATGAAAA 100
25 AATTNCTAGC CAGAGGCATT TAAGTGATTT CTTCCTAAGT GTTTGCTAAT 150
TCAATGCCAA GAACTATGAT GTTTATCNTT CTGATGGACA AATCAAGAAA 200
CAAAACAGAT ATAATACCAA GGGTAAAGCT GATATGACCC ACAACATTGT 250
30 CATTACTCTA ACTGTTAATC 270

(2) INFORMATION FOR SEQ ID :203:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

117

(xi) SEQUENCE DESCRIPTION: SEQ ID :203:

AACTAAGGCA CATTGCCCTT TTTGACCTTT CTNNNGNACT ATTGAAATCA 50
5 AGCTTATTGA TTAGGTGATA TTTTATAAC AATTGAAAGG GCAATATCAA 100
ATAATGACAT ATGAGAATTT TTTATTACAT ATTAAACTG ATTTTACTT 150
TACAAAANNG NAATTGCAA TTA 173

10

(2) INFORMATION FOR SEQ ID :204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :204:

CTGCTTCACC ATCCTGGCGT CTACCAGCCT GGTGNGGCTG GGTACTGTGN 50
25 ATCGTCTTCC TCAACAAATG CGAGACCTGC CAACCTGCAC TACACCACAT 100
CCGCNCAAGA AGAAGAACCT GCTGCTTCAT ACAACACGGG GAGGCCCTGT 150
CATTACATT ANTT 164

30

(2) INFORMATION FOR SEQ ID :205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :205:

118

GACCGCCCAN NNNCATCCAA AACTTCTAGG CACAATCTAT ACTGCTGCTG 50

AAGAAATTGA AGCAGTTGGG GGAAAGGCCT TGCCATTGAN TTTTGATNT 99

5 (2) INFORMATION FOR SEQ ID :206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :206:

GTACCTTGGG NNNNNNANNG GGAATGAGGT TCTACCACTC TGGAAAATTC 50

ATGCCTGTCA NTNTAANTNC AGGTGCCAGT TNNCNNTAGG TCGCCAAAGT 100

20 TGGGGTTAGN TGTTCNAA 118

(2) INFORMATION FOR SEQ ID :207:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :207:

35 CACACTANCG ACCAACACTT AAAAGNCTNC TCACACAAGN ATCTTTTAA 50

TAAAAATACC TCTTTCNTAA CTCCACTTTA ACTCCCTAAA ACCCATGTCC 100

AAGCCCCCAT CCTGGTCAAT AGTACTTGCC CAGTACTTTT AAAACTAGGC 150

40 GCTATGCATA ATACCCTCAC 170

119

(2) INFORMATION FOR SEQ ID :208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :208:

TTCAATGAAA TGCTTGATA CAATGATATA ACAAAGAAAC CCTAAGACAA	50
CGAGAACTTC AACTAAGTGC ACTCATGCAG AATCTCTGCG GGGAGAATT	100
TTTCTCGGGG AAGTAACCCT GCCTTTGAA	129

(2) INFORMATION FOR SEQ ID :209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :209:

CTTGCGTCA TTTTCTGTAC TTCTGACAGT GCCCTCAGAG TCTGCAGGTG	50
GATCCTTTTT TGCATGGCAT TAATTATATG AGCAGCCTCC TTCTGACAAT	100
CCAAATTTTG GCTCCAGAGT CATTTCTGAA NNTCTACACT TANGGNCTTN	150
AGCNTGCTCA TTCAAGGTNA AGGGGAGTTT TNAAAAATAT	190

(2) INFORMATION FOR SEQ ID :210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs

120

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :210:

TCATTGAGTC ATCCTTTTTG CCTGCTGCTG TAAGGTTTTT TTTCTTCTAG 50
10 TAACTGTATG ATCCAGAGCG ACCCAGCAAG GACTCAATCG ATCACCAACT 100
GATGCAGAAC TGTTTCATAT CTAGAAATG 129

15 (2) INFORMATION FOR SEQ ID :211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :211:

CTGTAAGGTT TTCTTTCTTC TAAGTAACTG TATGATCCAG AGCGACCCAG 50
CAAGGAATCA TATCGATCAC CAGCTGATGT AGAACTGGTT TCANATCTAG 100
30 AAATGGAANC NNNGNGTTTN TTCCTTAATG GACCCCCCN GGGGCNGAAT 150
GG 152

35 (2) INFORMATION FOR SEQ ID :212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

121

(xi) SEQUENCE DESCRIPTION: SEQ ID :212:

5	CTTAACCCTT TGGAAGGNTT GACTGTGTGA CCCGCAGCAA ATAATTCATG	50
	TCGAAAGATG AAAACAAC TA AGTTCATAAC CCCCTGCCCCG CCATTGACCT	100
	CCCTTTNAAA ANCGAGACCA AGACTCCATC ACTGGTTTCG AATTACATC	150
10	NAACTGCTAA GATTGATACA TTNCAAGTCT GCAAAT	186

(2) INFORMATION FOR SEQ ID :213:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 152 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :213:

25	CTTAAATGCC TGTGTGATA TCTTCTTTAA ACCTGGAGAG ATTGAATCAA	50
	CCTTTCTCTA AAATTCCTTT CCTTTGCCTC CTCCTCTAAC TTTTCCTCCT	100
	TTCNCGCTTT TCCTCAGGCT TTGNTTTTCC TCATGCTTTG CTTCACTCTA	150
30	TT	152

(2) INFORMATION FOR SEQ ID :214:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 290 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :214:

122

	TCTTCAGGAG AAGGGGCACC ACTGCTTTAA AAAACAATAC TCCNTTATAG	50
	ACTTGAACAT TTGCAGACAT TATGATCTTG CTTCCAACTC CCACCGTATG	100
5	TCCAGCAAAC TCTCGCATGT GGCCACTAGG AGGAATGCGC AAGAATGTTC	150
	ATATTACATA TTTATAACAT TAATAACTGG AAAAAGTGAA ATGCATGTCT	200
	GTTACAGGAA AATAGGCGAA TAATCAGATA TATATATCTA NNNCCGGGAT	250
10	ATTATTCAAT AGTGGAATG ATGACTACAG CTATACCTCA	290

(2) INFORMATION FOR SEQ ID :215:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 273 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :215:

25	GTTTCTTCCA GTACATCCAA GTTTAAAATT ATTAGCGAAA TGGTCCATGT	50
	TTTTTCAATT ACTGCTGACA CGATTCTAAG CTAAGTGAAG GGAAGATCT	100
	GAGAGCATGC TGTTTGGACT GTTGATGCAT ATTCATGATG TAACAGGTCC	150
30	TGGGCCTCAC TTTACCCCAT TCGTAAAATG GGGATAATGT CACCTGCCTC	200
	TTACCTACCT CAGAGGGATT TGCGAAGCAA ACTGTTAATC TTCGAAAACG	250
35	ACCATTACT TTTAGGATAT CAA	273

(2) INFORMATION FOR SEQ ID :216:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 118 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

123

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :216:

ATCTACGGCT AGGGAGAAAC AATGTTCTTA CATATTATGG GTAGTGAGAA 50

10 CATTATCTGT ATAACAGGGA ACTGTGATTA TTTAAAATTA TGCAGAACTT 100

ATTTCATCTG TGCTTTAG 118

(2) INFORMATION FOR SEQ ID :217:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :217:

25 GAGGCTGGTG GCGAGGGAGT TGTGGAGGAT AACAAGAAGA AAACAAGTCT 50

ATCACTAATG ACTTATTTTA CTTAGTTTCC ATTACGAAA CCCTTTTAAA 100

30 TACAAGGCAA CATTTTCACA GCTGAAAAAT TACAATAAA NGNNNTGATT 150

TACCACCAA AGCAATAGAT GTAGTTATGT ATAATCTATA GATAATA 197

(2) INFORMATION FOR SEQ ID :218:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

124

(xi) SEQUENCE DESCRIPTION: SEQ ID :218:

CTCGCGAGCA CTCGTCCGAG AGGTCCCATATA CNNNNNNNCC CAAGCCCCTC 50
5 AAGGGCCTTT GCCAATCTNG TCATTTTATG CCAAGTCCTC TAAAACGCAC 100
TCAGGGGTAT CTACATCGCA CTTGTACAGA ATATCAAGAT CTTATCCTCC 150
TATTTTAGGC TNCNAGGTCA AAATAAA 177

10

(2) INFORMATION FOR SEQ ID :219:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :219:

GAAATGAAAA AGAGAGCATT ATTGGAAGAA TGAAAAATAC ATCTCAGAAA 50
25 GAAACCTANT AGTTCAACAA ATTAAAAGAA AGAAAGAAAA AAAGCAAAAG 100
TNGGTNTCAG GGCTGGAC 118

30

(2) INFORMATION FOR SEQ ID :220:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :220:

GAGAGCCCAG CACGTCATCC CCTGATCTGA GTCTACTGAA CACCTGTTTT 50

125

ATGGACTACA CTGTCTTTTC CTTTGAATCC CCACTTCTCC TGGAAGTGTGTA 100
CTTGGACCAC CAGGAACATC GTAAGACACA ACCCAATACA CTCACCGCAT 150
5 TCAGACAACT GTCCAGACAC TGCCCTGACA CCACAGGGNC CCCTTTACAN 200
NGGTTGGNGG AAATATNNTT TAATCTCAGG CCA 233

(2) INFORMATION FOR SEQ ID :221:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :221:

20

GCACACAGAT ACCATCCCAC CTTGCTTTNT GACAGGCCAG CCACACAATA 50
ACCCTTTCCC TACTCACTAA AGCATCCCTA GGACACCAAC AATGAGGACA 100
25 GGCAGACTTA CCCCCGCCAT CTAGAGAGAA TGTCGTTATT ACCCATAAAA 150
CTCGACCACC CCCATATNCA CTNTTGGGTA AAAACAAACG CTAAACCTG 200
TGAGCCTGCC ATTCCTTTTT ACGTGTTAAT CAATT 235

30

(2) INFORMATION FOR SEQ ID :222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :222:

126

GCCAATNNNN NGGCGCGAGG GNNAGAGAGA ATGGCAAACA GGGACCCGGG 50

CCTTAGGAAT TGANTGAGGA CTAAATTTT CCCNGAGGGA GAGNAGTGGA 100

5 G 101

(2) INFORMATION FOR SEQ ID :223:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :223:

ACGGTGACTT TCCATCCCTT GAACCAAGGC ATGTTAGCCT TGGCTCCAGC 50

20

ATGTCGTCAC CATTCCAACC AGAAATTGNC ACAAATGCTA CTGGTCGGGT 100

TGACCAATTT TCTTAATGAA GTGCTGACTT CCTTAACAAT TTNTTATATT 150

25 TNTTCGACTG TAGGGCGCTC ATGAATCCAT TTCGTTAACA CCGACAATTA 200

ATTGTTTCAC ACCCAGTGTG CAAGCCAGAA GGGCATGCTC TGGGTCTNCC 250

CATTCTTGAG ATACCAGCTT C 271

30

(2) INFORMATION FOR SEQ ID :224:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :224:

127

AGTATTATTT ACTNGGTCAT CTGGGAACCT TAATGTGATT TATTTTGACA 50

ATTACTGTGG CACATGTTTA ATCTGCAGCT CCTGGCGACT ACTGTGCTTA 100

5 T 101

(2) INFORMATION FOR SEQ ID :225:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :225:

TTCATTCCCT CCAGTGCNCG NNCATGCGAC ATATACAGGN NNTGTACCGT 50

20

AGGCGCTANT GTGTGGTACT CTGCCACGNN ANACCNCNNC TCGTCTTGAA 100

GACCCTGTTA ANTTTGGTGA AAATAACTTT CCANATTTC A 141

25 (2) INFORMATION FOR SEQ ID :226:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :226:

ATTTTCTTAT ACTCCTCCCA CAGATGAGTT CACAAATACA AAAANTGGTG 50

40

TACATTTATA CTCAAGNACA AATCTCCAAC AGCCAAGTAA TTATAGTTTG 100

TTCTGTTATG TGCAAAGTAG ATTATTTTCAT ATTTACTTGG TATGGAAAGC 150

128

AGAGTACAGG CTCAATGGAC AATAATCATT AAACACACAT TATNTTTAAG 200
AAAANGCTGT TNNAAAAA 218

5 (2) INFORMATION FOR SEQ ID :227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :227:

GAAAACTTTA TTTGTCCACA CCAGGATTAC CGAACAGAAN NACNNGGTGG 50
TGAGAAGTTG GTATTNATAG CACCTTATTT ACATGATGGA CTTGAGGAGG 100
20 CAGTTAATCC TATGGTTGTG TATCACAACC TTTTATTAGC AATGCCATCT 150
TCGTCTTGCC TCCNCCCTAC TTGAATATCC CTTACGGTCA ACANCCCNCG 200
25 GGGTTGGGC 209

(2) INFORMATION FOR SEQ ID :228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :228:

TTTNNCAANC CAAATGGTTA TTTATTCTAA AACTGGAAGC TACTTTGCCT 50
40 ANCATTTTCG CCAGAATGGT GTAATGNNNA CAGGGGAGGA AAAAAGTTAC 100

129

AGATGTAAAC AATGACACAG TTACATTTTT TTTTAAATG GTAAAACCCC 150

TTTTTACTGG NCNTTCCAGA ANCTTACAG 179

5 (2) INFORMATION FOR SEQ ID :229:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :229:

AGTTTAATCT CANNNNNNNA TGTCAAGT TATTGTAGCA GTGAAACAAT 50

GAGGGCATACT ACTATATNGA AAAAAAACC TCCTCCCTNA TTCTCAGCC 100

20 AACCACAGGC TTCTGCCCTG CAAAGATCAC CAATGTCAAT AGTTTGGTAA 150

TACACCATCA TAAAGGNTCC TAAATTCATC TCTA 184

25 (2) INFORMATION FOR SEQ ID :230:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :230:

GAGACAGATG TANNNAAAGT TCAGAATACA ACAGTTAAGA CTCAGTTTTC 50

TTTTTAGGTT TAGAATTGA GAGCAAGTAT TGNTATGGTG AGCTGTTTTA 100

40 GTGCAAACAT TGTGAGTAT GTTGTCAAAC GTCTAAAAA 140

130

(2) INFORMATION FOR SEQ ID :231:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :231:

CGGAGACTTG TCCAGAGAGT TGTCTCTTNT NNGTTGGGGG CCGTCCCGCT 50
15 CCTAAGGCAG GAAGATGGTG GCNNNTNNGG ACGAAAAAGT CGCTGGNGNN 100
NATNAANTNT AGGCTCNAAN TNNTTATGAA AANTGGGAAG TAANTNNTCG 150
GGGGTAAAAG NAANATNNGA ANATGGAT 178

20

(2) INFORMATION FOR SEQ ID :232:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :232:

GAGCCAACGC CACNNNNNAG NTGAACCACA CTCACGAAA AAACNCNTAC 50
35 CGTCGTCNTA ATACNNANTC TTCCCATACA AAAATCGTCC NTNTAAATNT 100
NNTAAACCAA TTCACAGCCC ACAGAACNAA TCAGTAATTT TATANCTTCN 150
NCGAAACCAC ACTTATCCCC ACCTTGGTCT ATTCATNACC CGGATNGAGG 200
40 GCAACCANGG 210

131

(2) INFORMATION FOR SEQ ID :233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :233:

ACTGTGCGAG TAGCTTNAAA ANNNNNNNNN NNACTCAGTT TNATTTATAC 50
AAAAAGAAAG GGGTGTGNAG TCCATGGTGT TGTACAGTNT NTAATTAGNC 100
CANNACGAGA AAANANATNN NNNTNNNAAA NNNTGAATTA TGGGGTNAGG 150
ACTNTCTNAC NTTCAAACNA NTATTNCACG TAAAAACAT CACAGTGC GA 200
AGAAAGNNAN CNCANNTAGA GCANGAAGAC ATCAAAAGCC AGCCGGG 247

(2) INFORMATION FOR SEQ ID :234:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :234:

AAACACCAAA NAAANNNNNC NAGCAANAAA GTGGAAGACT AACCAAGATT 50
GTGGACATTG GAATGTTTAC TGTTATTCTG TGTAAGAAAA CAACTNACAA 100
AAAAGAAAAA TGNCAACAA AATTGTTTCC CGGCNAGGCT GNAGGAAACC 150
NGGGGGAAAN TGCCNGGGC 169

132

(2) INFORMATION FOR SEQ ID :235:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :235:

GCANCAACANA AAGGAGACGN NANAGCAACG CAGAGATAGC CATCCAGATA 50

15

G 51

(2) INFORMATION FOR SEQ ID :236:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :236:

CAAGTGTAAG TGCTTGCACC TCTCTNCCTC CCCGANTGAA CTCTCTGATC 50

30

TCAAACCTTTT TTAGGAAAGC CAGATTAAAA GCAGACGTAC CTAAATNCAA 100

A 101

35

(2) INFORMATION FOR SEQ ID :237:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

133

(xi) SEQUENCE DESCRIPTION: SEQ ID :237:

5 CATTATAAAA CAGCCTAACT TCCCTTATGC CATATGATTG CCTTAAAAAG 50
ACCAGATCTC AAGGAAAAGA TCATCAAAGA GCAGAGATCT TGAAGCGGCA 100
CAGTTTTTCCA GCAGTTTTTCG TATTNTTTTT TATTACGAA TGCCATACTC 150
10 TGTTTT 156

(2) INFORMATION FOR SEQ ID :238:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :238:

GCAGNCTAAT TGTGAATCTA AGAACTACT CATAGACATC CCACCCTAAT 50
25 GATTTTACCT NNAACNTTGT TCCTTCATCA TAGAACCCTA GCAACATCCA 100
CCTCCTGTAG CACGAAACGA ATCAAACAAC CCCCTGGATA ACCTCTCA 148

30 (2) INFORMATION FOR SEQ ID :239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :239:

GAGTTTTAAC TTAATCACCT CTTTAAAAGA CCTGTCTCCA AATACAGTTA 50

134

AATTGAGGT ATTGAGGGTT AGGACTTCAA CATGTGAGTT TGGGAAGGGA 100
 AGCACAAAAT CAGCCCCTAC CATGGTATAT TTATCATTGA TACATTACTA 150
 5 TCAACTAAGC TCAAGATTTT ATTCAGATTT GACTAGTTTT TCCACTAAGG 200
 CCCTTTTTCT TTTCTAGGNT CCCACAGAGG ATACATTACA TTTACTTACA 250
 TCTTCTCT 258

10

(2) INFORMATION FOR SEQ ID :240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :240:

GAGCATTATT TGATGCAGAA GTTGAAAAAC AATAGACTCA AGAAAGAAAA 50
 25 CAAACCAGTG ATTCCCTTC CTCAGATACT GGGACTAACA GCTTCACCTG 100
 GTGTTGGAGG GGCCACGGAG CAAGCCAAAG CTGAAGAACA CATTTTAAAA 150
 CTATGTGCCA ATCTTGATGC ATTTACTATT AAAACTGTTA AAGAAAACCT 200
 30 TGATCAACTG AAAAACCAAA TACAGGAGCC ATGCAAGAAG TTTGCCATTG 250
 CAGNTGCAAC CAGNGGAGNT CCTTTNAAGN GNAACTTCTN GNATAATNNC 300
 35 AAGGGTNAAC NTNTTTNNAA ANNNGCCNAA NCNNGATTTT GNACNCCCTT 350
 TNNCATTGGC ATTNANTGAA AAAAGTT 377

40

(2) INFORMATION FOR SEQ ID :241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs

135

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :241:

GGNGCACTGN TCCGAGAGCT TTTTNTCTG AAGAATAGCA TCTTTAATGA 50
10 GTGTNCTAAT CCTTGTCATC TGAAGTTTTC AAATATATTT CCCAGGGTCA 100
GAACAATACA GAGA 114

15

(2) INFORMATION FOR SEQ ID :242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :242:

CTCAAAATNC TGTGACAAAT TTNNNNGGTC AAGTTGTTNN CCATTAAAAA 50
GTACCTGATT TTCAAAAACC TAATAACCTT AAAACCNCCC CACGNAAAAA 100
30 AAAAAANCNA AAGNGGGCCC CC 122

(2) INFORMATION FOR SEQ ID :243:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

136

(xi) SEQUENCE DESCRIPTION: SEQ ID :243:

5 GAGAATGGGA AGCCTCATTT TGGGGACAAG AACCTGTACA AGGATTTGTG 50
 ATGAACTTTT CCAATGGGGA AATTATAGAC ATCTTCAAGC CAGTGCGCAC 100
 NTATGATATG CCTCATGATA TTNTTGCATC TGAAGATGGG ACTNTGTACA 150
 TTGGNGATGC TCATCCAAAC C 171

(2) INFORMATION FOR SEQ ID :244:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :244:

AACTTTACTG TCAGATAATA AAATTAGGGC TTTCTCTTAA AGGGCTTCTT 50
 25 TAAGAGAAAT ACAGAGTGTT TGGTATNTGA GAGAAAAAAA GTTAAACAG 100
 GACTTTCAAC TTAATCCAGA CTCCTAACA GTGTTTACAT GTGAGGGAAA 150
 CTCCTTTAAG TAATGCGTAG TGTTTTATTT TTACCATCAT TGGNGACAAA 200
 30 AAAAACAAAA ACATAAACAT CTNANGTGAA ATATA 235

(2) INFORMATION FOR SEQ ID :245:

35

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

137

(xi) SEQUENCE DESCRIPTION: SEQ ID :245:

	GGCCTAGCCT GCCATACCCT TACGAGCAGG CTCAGTGATT AGACTTTGAG	50
5	TCTAAGTTAA AAACGCCCTG CCCCCTTCTC GCAGGCCACC TACACCGTNN	100
	TTTTATCGAT TTGATAAAAC CACCAGCCTA CTCATCAAGN NGCACCCTGC	150
	NTNTACNTCT AACCNATAACA TNACNGCGGC CACCTACTCA TGCCCTANTG	200
10	CAGCNCACCC T	211

(2) INFORMATION FOR SEQ ID :246:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 194 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :246:

25	GGCTGAGAAT CCTTGAGCTT ACCATTTGAT ATTTCTATAT TATTTAAGAA	50
	AAGTCAAAAAG ATTTTGAAAA CAGCAATAGA AGTAAGATCC TTTAAGCTCT	100
	ATTTGCAGCC CCTAAGAAAA GTGATGAGGA CACTGTGCAT GCCCATATGT	150
30	GAACATGGTG GTACCTTAGG NATTTCCCTT TNTCNATGAA TATA	194

(2) INFORMATION FOR SEQ ID :247:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 249 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

138

(xi) SEQUENCE DESCRIPTION: SEQ ID :247:

	GCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT	50
5	GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG	100
	CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT	150
	GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA	200
10	GCCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCCT	249

(2) INFORMATION FOR SEQ ID :248:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 248 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :248:

25	GCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT	50
	GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG	100
	CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT	150
30	GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA	200
	GCCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCC	248

35 (2) INFORMATION FOR SEQ ID :249:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 82 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

139

(xi) SEQUENCE DESCRIPTION: SEQ ID :249:

GGAGGGGACC GCAGCATCCA GCCCTCTAAG GCCGGGCAGC GGTCGCGTTG 50

5

GGGCAGAGCG CAGCGCAAGC AGGCTCAGTG TA 82

(2) INFORMATION FOR SEQ ID :250:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :250:

20 GGGGCCCTCA GGACATCCAC GTGAGCGTCT GCCCAGCTGC ACTGATATTG 50

TNTTGCAAAT CCAGATTTGT TGNCATTACT GATGGGCGCG TGAAACCAGN 100

GAGAGATGCA CAAGATTTAC AGGCC 125

25

(2) INFORMATION FOR SEQ ID :251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :251:

GGCCCAGAGG TCCTTTACTC TTACGGNACA CCTTAGCCAC ATTCACAGGG 50

40 AATGNTCCAG CACTCAGGCT CCTTCCCATN GGTTTTCAA AGCGCGTTTT 100

TCTGGGGGAG CGGCCGCCTT TAGTCGACCC 130

140

(2) INFORMATION FOR SEQ ID :252:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :252:

GAGAAGGCTG GAGAAAAACC ATCCACACAT AAACAATNGN ATTTACTCNA 50
15 AAATNAAGTA CAGGTTTCAG GTATTTAAAA TAAATAAAGA AAAATCTCGT 100
TTCCTTTGGC ATCTTTAGAA AATAAACTAA GCAATAAAAG AGGTGATTGT 150
ATAAAGACAT GCGTAAGCAA ACATATGGGG AAAACCAGCA ACTTGTTTTT 200
20 ATGNGATAAT ATCAGC 216

(2) INFORMATION FOR SEQ ID :253:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :253:

35 GGAGAAGGAG GCTGATTGCG TACATCCAGC AGTTACAATT TTTAAAAATT 50
ACANTNNNNC NNTTNGATTN TTAATNTANG TAATTTCTT CCAAAGAAGN 100
TTCACATGTA ATAAGTAGAA ATTCTGTATA GGAAAAAGC ATTAAAAATA 150
40 TANATACNGC TTCATNCGTT GGGAACCATT AAAAGTAATA TAATNAGCTT 200

141

TTTTCAGAAG GATCTTTTGT AGCAGTGNTT ATGAATGNAC CCGCAAAT

249

(2) INFORMATION FOR SEQ ID :254:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :254:

15 GACCCCATTC TATATTATNC GTNNNGCGAT TTTTGTAGCCA CCCTGAAGTT 50

ATATTTNTAT ACCNAGGCTT CGAATAATCT CATCNGACTN ACCACCCTNG 100

GAAAAAAGA ACCGTTTGAT ACATAGGNAT GNTNAGCTTG ATATCAATNG 150

20 CTCCCTGGGN TTCTTG 166

(2) INFORMATION FOR SEQ ID :255:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :255:

35 CCAGACCAAC CGCCTGCAGG AGGCTCTGAA CCCTCTTCAA GAGCATCTGG 50

AACAACAGAT GGCTGCGCAC CATCTCTGTG ATCCTGTTCC TCAACAAGCA 100

AGATTGCTC GCTGAGAAAG TCCTTGTGGG AAATCGAAGT TGAGGACTAC 150

40 TTTCAGAATT TGCTCGCTAC ACTACTTTGA GGATGCTACT CCCGAGCCCC 200

142

CTTCTNTTGT NACAGACAGC AGA

223

(2) INFORMATION FOR SEQ ID :256:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :256:

15	GGAGAAGAAG GAGCAGGAGG TGATGCTACT GACTCAAGTC AAACAGCTCT	50
	TGATAATAAA GCTTCATTGC TCCATTCAAT GCCTACTCAC TCCTCTCCGC	100
	TCTCGAGACT ATAATCCATA TAACTATTAA GATAGCATCA GTCCCTTCAA	150
20	CAAGTCTGCC CTCAAGGAAG CCATGTTTGA TGATGATGCT GACCAGTTTC	200
	CTGACGATCT TTCCCTAGAT CATTCTGACC TGTTGTAGAG TTGTTGAAGG	250
25	AGCTGTCTGA CCATAATGAG CTGTAGAAGA AAGAAAAATT GC	292

(2) INFORMATION FOR SEQ ID :257:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :257:

40	AAGGAGCAGG AGGTGATGCT ACTGACTCAA GTCAAACAGC TCTTGATAAT	50
	AAAGCTTCAT TGCTCCATTC AATGCCTACT CACTCCTCTC CGCTCTCGAG	100

143

ACTATAATCC ATATAACTAT TAAGATAGCA TCAGTCCCTT CAACAAGTCT 150

GCCCTCAAGG AAGCCATGTT TGATGATGAT GCTGACCAGT TTCCTGACGA 200

5 TCTTTCCCTA GATCATTCTG ACCTGTTGTA GAGTTGTT 238

(2) INFORMATION FOR SEQ ID :258:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :258:

GGAGAGAAAA GTTCCTGAGT GACAGAGAAA AAGAACAAAA AGCTGCAGAA 50

20

GGCNTCAGCA GAGGCCACTG CTGGCCCTGA GGCTGCACCA AGTGACGAAG 100

AACCGGCTCC AAGCATTCGT CACAGCACTA ATTTAAA 137

25 (2) INFORMATION FOR SEQ ID :259:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :259:

GCGCGACTTT TAAGGGATTT GCNGTGATGC CTGTTGACCC AGTGCCTTCC 50

TAGCCGGGAA GGGGCTCGGC TGGAGTGNN AAGGCTCAGAA AAATTTGCGG 100

40

AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT 150

144

TTTTGGACAG GTGGGTGCGG TGACCTGGT ATGTATTTTT CGTGTTACAT 200
CGCGCCATCA TTGGATATGT TAGTGTGTNG GTTAGTAGGT C 241

5 (2) INFORMATION FOR SEQ ID :260:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :260:

GCGGACTTTT AAGGGATTG CNGTGATGCC TGTGACCCA GTGCCTTCCT 50
AGCCGGGGGAA GGGGCTCGGC TGGAGTGNN AAGGCTCAGA AAAATTTGCG 100
20 AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT 150
TTTTGGACAG GTGGGGCGGT GACCTTGGA TGTATTTTTC GTGTTACATC 200
GCGCCATATT GGTATATGTT AGTGTGTTGG TTAGTAGGTC TCGTATGA 248
25

(2) INFORMATION FOR SEQ ID :261:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :261:

GGATCTTTCA GGTGATGAAA TAGTTCTGTA TCTTGATTTT GGCGAATCTA 50
40 CACANGTGAT GAAGTAACGT GATAAAATGA CATAGACCTG TATGCCTACT 100

145

ACAATACAGT ATCAAAACCA GGGATTGATT CCTGGTTCTT TTCCAAATCC 150
ACTTCCCAA CTTATGGTAA GGTAATATTA AAAAGGCACC AAAGAGCCCT 200
5 GATCCCTGGA TAAACAGGAT CATTTCAAAG NNGTTTATA 239

(2) INFORMATION FOR SEQ ID :262:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :262:

GCCGGGTGAT GGCCAGGAAG GTGCCCTCTG TTTTTGTAA AACAGCCATT 50
20 GGCCTTTGTC ATTGAGTCAC CACCTGCAGG GCTTGGGAGT GAGCGTTGGG 100
TAGGNTCAGG CCCCCAGAAC CGCCTGGGTA CTCACCGCTA GCA 143

25 (2) INFORMATION FOR SEQ ID :263:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :263:

GGCGCTCAGC CTCCCCAAGG ACAAGCTCCT CCCCCTGTAA TACCTCCTCC 50
TAACAGCCCG ATATGGATGG CAACTTACCA AACACAGTGA GCCGGGACTC 100
40 TAAAAAATA TAGCAATCCA GATAGGCTTC GATTTCCTGT GACACTCTGA 150

146

AGACATGAAA GTAGACATCG AAAATGAAAA TANTTATNNA AATGAAATGT 200

TTGGAACCTT TAGCACAGAT TTGTTTGGGA AGACACGGTC TTTTAG 246

5 (2) INFORMATION FOR SEQ ID :264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :264:

GGCTCCATTA AGGACCAAAT TNATGCTACC ACTAAACAAA AANNTATAGT 50

CTGTGTAA TCGTATGCTT TTAAAGGTA TTAAAGATT CAACTAGCTT 100

20 TAAAGAGGCT GAGCAGCTCA GGAAGCCTGT AATGTGACAT AACTCTTTGG 150

ACCTGATCTT GATGTTCTGC TGTGTNAGT CTTGAAGAGC GATNTGAT 199

25 (2) INFORMATION FOR SEQ ID :265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :265:

GGTTTCAATC GTCCATCCAA GATACAAGAG AACGCATTGC CACTGATGCT 50

TGCTGAGCCC CCACAGAACT TAATCGCCCA ATCTCAGTCT GGTACTGGTA 100

40 AAACAGCTGC CTTCTGTCTG GCCATGCTTA GCCAAGTAGA ACCTGCAAAC 150

147

AATATCCCGT GTCTTCTCTN TCCCAACGTA TGAGCTGCCC TCCAAACAGG 200

AAAAGTGATT GAACAAATGG CAAATNTTAC CCTGAACTGA AGCTG 245

5 (2) INFORMATION FOR SEQ ID :266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :266:

AGGAAAAGAT GGGAAATATGT TTCTTTCCTT TGAGAATTCA CAAAANGGGG 50

TCAAAAACAA AGCAATGCTG AAAGCGAACA TCCATTNGC CTGCAATTCA 100

20 AGGCGAAAAT CCAAAGGCAT C 121

(2) INFORMATION FOR SEQ ID :267:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :267:

35 GGGTCGCTCT CCCCCCTCT TTCTTCGGGT TGTGTGCGTC TCCGCTTTCG 50

TGATGTGAGG AACTCTGGGG TGGGCGACGG GTCCAACCTCG CGTTGTCATC 100

TCCCAGGTTG GTACACCCCC CCCCCGTTTC CCCAGCCACA CTCCACGGCC 150

40 AGGGTGGAGG CAGATGTCT 169

148

(2) INFORMATION FOR SEQ ID :268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :268:

TCGCAGGAGA GGAATTACAT GCTCATCCTA GAAGGGGGGG CTGACTGCAG	50
GTGTTGCTGG GAAGCCTCTC CAGGCCTGGA GCTGGAGTAC CCGTCCTCAG	100
CACTGCCAGC AGAAAAAGTT GTGATTCAAG GAAAGCACAT TGAATGCATT	150
ATAGCAATCC CAGACCTAAG TTCGAAGTTG CTTTGTAACA AGTGCTGCCT	200

(2) INFORMATION FOR SEQ ID :269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :269:

AGGGGGGCGC AAGAGAGAAG AACTTCACAC TTCTTTATTG CTCAGCCTAG	50
ATAGCAGCAG CTGGGAATAC GTAGGACAAA CAGGACGTCG AACAAATTAC	100
TCCACTATAT TAATATTCAC TACACCACTT ATTCTTTCTT GAATTGTAAA	150
CACTAAGTGT AGT	163

(2) INFORMATION FOR SEQ ID :270:

149

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :270:

TCACACTTCT TATTGCTCAG CCTAGATAGC AGCAGCTGGG GAATACGTAG 50
GACAAACAGG ACGTCGAACA AATTACTCCA CTATATTAAA TTCACTCACA 100
CCACTTATTC TTTCT 115

(2) INFORMATION FOR SEQ ID :271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :271:

CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA 50
GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNNGN 100
NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC 150
TGCAGAAATN CCTATGTGAC TCTTATAA 178

(2) INFORMATION FOR SEQ ID :272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

150

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :272:

CCCAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA 50

GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNNGN 100

10

NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC 150

TGCAGAAATN CCTATGTGAC TCTTATAA 178

15 (2) INFORMATION FOR SEQ ID :273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :273:

CTCTAGTAAA AATGTTTGAG GAAACAAAAA TGGGGAAGAA GATCAGAACA 50

AAAANATTGT TAACACTGAC CGTCCTCATG CAGGTAGGCT ACTACCAACG 100

30

CTGGTTGTTA CTCCAGGAAA ATCGAGGTGA ACATC 135

(2) INFORMATION FOR SEQ ID :274:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

151

(xi) SEQUENCE DESCRIPTION: SEQ ID :274:

	TGTCGAGGAG AAGAAACCAC TTGATAACAC CCCGCGACAT CGTGGGGCTG	50
5	CTTGTCACAN GAAAGCACCA TGTTGCAAT GGATTGCTGC AGGTGCTGCC	100
	GTTGCCTCCT CAGGGTCTGC TGAAAGTCAT CTTCTAGGGT CTGAACGACA	150
	TAACGCAGGA AAAGGACTCG CCCAGGCAGA GTTTGTCCCT CTTCTTCAT	200
10	GACATAGGTG AGCAGTTTCC AGTCCCACTC C	231

(2) INFORMATION FOR SEQ ID :275:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 170 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :275:

25	TCGCAGGAGA AGAAACCTNG TTGCTCCACA ATGCAACCAC ACTGATTTTC	50
	TCTTTTCTCT NNAGTTNTCC TTGTCTGTAA CAGGAATGTC CCTTACTATA	100
	GCAGGCGGAC ACGGCCATGG GTCAAGCACC CTGCTTCTGG AACTTGNNNG	150
30	NCGTNCCCAC CATTGATTGA	170

(2) INFORMATION FOR SEQ ID :276:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 315 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

152

(xi) SEQUENCE DESCRIPTION: SEQ ID :276:

	ATATGAAGGA GGAAATGGCT CTCACCTTCG TGAATACCAA GACCTGCTCA	50
5	ATGTTAAGAT GGCCCTTGAC ATGAGATTGC CACCTACAGG AAGCTGCTGG	100
	AAGGCGAGGA GAGCAGGATT TCTCTGCCTC TTCCAAACTT TTNTCTGAAC	150
	CTGAGGGAAA CTAATCTGGA TTCCTCCCT CTGGTTGATA CCCACTCAAA	200
10	AAGGACACTT CTGATTAAGA CGGTTGAAAC TAGAGATGGA CAGGTTATCA	250
	ACGAACTTC TCAGCATTAC GATGACCTTG AATGAAAATN GTACACACTT	300
15	AGCGTAGCAT ATTNA	315

(2) INFORMATION FOR SEQ ID :277:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 209 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :277:

	ACGTTCTGCG CCTTCCTAGG AGAGTCTTAC AGTGTTGAGA TTTCACAAGC	50
30	AATGCGAGTG TAAAATACCA GCTCTACAAG AAGCTAGGCT CTGTGACGGC	100
	ATAGTTTTCA GTAGCTTTAT CACAATGAAA CGAGAATTAT ATGACATGGT	150
35	AGCAGAAATA GGCCCTTTCG TGNGCTGTTT TATTNCTCG GATNGTAGAT	200
	ATAGTAATC	209

(2) INFORMATION FOR SEQ ID :278:

40

(i) SEQUENCE CHARACTERISTICS:

- | | |
|--|----------------------------|
| | (A) LENGTH: 107 base pairs |
|--|----------------------------|

153

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :278:

AAGACATCCT AAGCTATGTT GAGGAGGGAG AAGATCTGAG ACTCAAGTTC 50
TGCTGTAAAC CATGAGGTGA TTTAGTAGCT AAGTACGCCT TAGCCTTTTA 100
GAGTCTT 107

15 (2) INFORMATION FOR SEQ ID :279:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :279:

ATGAAGAGAA AACCATCCTC CCATATGAAA ATATTTGCAG TAGGAGAACA 50
CAGTGCAATA GGCTCCAAA ATGGCTTTTA AGACCTTTGG NGGGGCAGTT 100
ACTACTGCTT TAAAGCCAG GTTAAAGTAT ACTCTAAGCA AAGATGACCG 150
TAGAGCAGCT AGCTTCCTTT TCTATAANNA TAGGGAAAGC TCTCTCCATC 200
GTCCATCAAA TCAGCTCTAG AAGGTTTTTC TTTCCCNCT ATAAGTGCAC 250
AAAGGGGAAA CACTGATTTC AAGCTT 276

35

(2) INFORMATION FOR SEQ ID :280:

40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 185 base pairs

154

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :280:

	AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA	50
10	CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT	100
	TAAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATACA	150
15	GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAAT	185

(2) INFORMATION FOR SEQ ID :281:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 186 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :281:

	AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA	50
30	CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT	100
	TAAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATACA	150
35	GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAATA	186

(2) INFORMATION FOR SEQ ID :282:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 198 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |

155

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :282:

TGTGGGCTCA GTAATGTCCC CGCTGATGAC AATTTCGAGA GTCCATGTTT 50
TATAGAAACC TTGAGGTCGG CCAGCCGTGT CTTGGCCAAT GAGATGTAGT 100
10 TGTGAGGAGG GGGCGTACTT GGGGACCAGG GGTGGGTGGA GATGTGCCCT 150
GTAGGCACAG GGAGACTCAA AAGCAGGAGT TNTGAAAGCG TAAATGGG 198

15 (2) INFORMATION FOR SEQ ID :283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :283:

AGAAAAAGGT GAAGCGAAGC CCAAGGACAC CATGCTAAGG GCAAAAGTAA 50
GAGACAGTCT CAGAACTGAG AGAATCGTGT CTTCTGCTTT TTGAAGTAGA 100
30 CTGTCACACT CAGGCAGCCT GTCAATGCTG AATGTTAGGA CTTCTGTCTC 150
CGCTGGAGAC ACGCCTGGGC AAGTCAGCGT TTAGTGTTTG ACAGCTTTCT 200
35 CAGCTCCCTG ACTCCGTTTA CC 222

(2) INFORMATION FOR SEQ ID :284:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

156

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :284:

ATGGATCAAA CTACCTCTAT AATGAAGACT GTTCTCAAAA ACGCGAGGNA 50
ATGTGNGACG ACACTGACCT ATCAGACAAG AGGGCATGCC CCCCTGGCCA 100
CCTTTGNCGC TGTTTNTGCA ACGTTCGCAG TGNTACTCTG CGTGAACCGG 150
TAGACTGCTT GG 162

15 (2) INFORMATION FOR SEQ ID :285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :285:

GGATCCANGC AAAGCCCACT CCTCCAGGGT GAAGTTTTTC TCCCGCGACA 50
GACAGCAGAC TCGAGCC 67

30

(2) INFORMATION FOR SEQ ID :286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :286:

157

GGTCGGATCA GGTCACCCCG CAGCAGCAGC TCTCGAGAGC TGAGGCACAA 50
GGCAGGGGCC CGGCTGTACA CCTGCAGGAC CCAGGAGAGC CTGTTGCAGT 100
5 TCTTGTCCGA AGCGCCGAGA TAGCCACTCA GTGTCCCTGC AGCAGGAGCA 150
GAA 153

(2) INFORMATION FOR SEQ ID :287:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :287:

20

TACTACGGCT AAGGAGAAAC AATGTTCTTA CATATCACGG GTAGTGAGAA 50
CATATCTGCA TAACAGGGAA CTGTGATATT TAAAACAGC AGAACTTATT 100
25 CCATCGTGCT TTAGAAATAA CTGTATACAG TGTATAAGT TGAAAAGAAC 150
TCAAAATAAC TGATATAAAT ACATCTATGT ATTAGAATTT AAAAAAGCTG 200
CTTTCTGTGA AGTCAATCAG CTATATTAAA AATGACACAA ATCCAAAACC 250
30 GATGCATGCC ATATANAAGG GACATTGNAA GTCCGCTCGC TGC 293

(2) INFORMATION FOR SEQ ID :288:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

158

(xi) SEQUENCE DESCRIPTION: SEQ ID :288:

AGGGTAAATG TACGTTGTTG AGTCACAGGC CTGCCAGACC TCTACTACCT 50
5 CATTGTCCCC TCCGGTGACC AGTTCTGCCG TCACTGTCAG GAGAATGCCC 100
GTGTTGAATC ACTG 114

(2) INFORMATION FOR SEQ ID :289:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :289:

20

ATGAACCACT GCCCGAGGTA CCCGGGTGTG GACCAGAGAA GTTTGCTGGA 50
AAGGACGTTG CCAGGACTTA CACGTTTACA GATCCAGCAA CTGCTCTNCC 100
25 CAGTGCCACA ACCATGGGGC GCCAACCACA AGCAGGAGTG CCACTGCCAC 150
GCGGGCTGGG TCCCACCCNA CTGCGCGAAG CTGCTGACTG AGGNGCACGC 200
AGCGTCCGGG AGCCTCCCTG TCCTTGTGTG GGGTATGGNG CTCTGGCGTT 250
30 GNGCTGGTTA CCCTGTAGGA GTTANTGNCT ACCGGAAGCT 290

(2) INFORMATION FOR SEQ ID :290:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

159

(xi) SEQUENCE DESCRIPTION: SEQ ID :290:

AACCGCTCTC CACACCGCTC CCACGAGCTC CAAGCTTAAA CGTCCAGATN 50
5 NACTTTGTTG CTTTGCTGAT TTTAACAGCT TGATTCTAAG CNCTTACTAG 100
TATCATNTGT GGCAGGACTT GNTCCATATC AGTGTTACTT TTGCTACTGT 150
TTTGTAGAAC GATGTACATG AATGAGCCT 179

10

(2) INFORMATION FOR SEQ ID :291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :291:

TCTTTCATTT TGNCTGCCAA TCATTGTCAG AAATTTAGGG AAGTCAATTG 50
25 TGCCATTACC ATCGGCATCT ACTTATTAAT TATGTCCTGT AACTCTGCTT 100
CTGTGGGATT CTGCCCAAGA GATCTCATT CAGTTCCCAA TTCTTTGTTG 150
TTATAGTACC ATCACCATTT CGTTAAATAG TGAAAGAGCT TTTTGAATC 199

30

(2) INFORMATION FOR SEQ ID :292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :292:

160

GGAAGACCAT TCTGATCATC CTCACTGACG CCA¹GGCAA GAGGGTGGTT 50
TTCCTGAAGC AGCTGGCTGT GGCTTATACT CGTGACTGGA CCTCTGGNCT 100
5 CAATTGAGTT CCTCAACGAA GACCACACCA GAAATTGTCA TTGCCACCTC 150
AACCGAANNG ATATTACAAT GTAAAAA 177

(2) INFORMATION FOR SEQ ID :293:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :293:

20

ATTGGTTTTCTCATCCACT GAGAATGCTG CTGGTTACTG CAAACGTTCA 50
CCAACCANAG CTTTGGTCCA TACAGCTTTC TTCTAGATTN GGAGACTCTC 100
25 AAGGACAGCA GGNGCTTTAA AATCCCTGGA CTGTGTTGAG AGGGCTTCTT 150
TAGGCTTTTC ATGATGTGAA TAGCCAGTCA TGAAC¹TTGN GTCTGTTTCT 200
TTTAGGCTCT TTTTGCAGCA GCAGAGCCAT GCTATNGAAG GAGTGAGAAC 250
30 CTATGCGAGN GACCCNGTGN TTGNACTGCG CAGGGAGCTT GCGGT 295

(2) INFORMATION FOR SEQ ID :294:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

161

(xi) SEQUENCE DESCRIPTION: SEQ ID :294:

AATGATCCTT TTTTCGCTCT TACCTATAGT ACAAGTCCAT GATACTACTG 50
5 CATATTTTAC CATTTTGNA AACTGTGAG 78

(2) INFORMATION FOR SEQ ID :295:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :295:

ATTCTGTACC TGTTCTGAAC CTCGCCATAA GGGACTTGCA GCTTCGATT 50
20 GCTAACCTGA AATTCTGCTG CTGCCATGGA ACAAGCCTGG GCTAGCTTGG 100
GGGAGGAGGA GAGACCATGT GGAGTAGAGC CAAGCTCTGG ACATTGAGA 150
25 GAGCCCGGTA ATA 163

(2) INFORMATION FOR SEQ ID :296:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :296:

AGCTTAGAGC GGAACGGGTT CCACGTGCGG TACTCCTGCT TCACGCCGCC 50
40 CTCGGTCACC GTGACGCGCC TCTCGCCGTA CACAGACTGG CCCGGCACCA 100

162

TGTTAGCGTG ACCAGCGCGT CCTCCGCCCC GCGTNAGATG AAGAGGCCCT 150
CGTGCCGGTG CGCTCCACCG ACACCACCAT GGCCCCCTC 189

5 (2) INFORMATION FOR SEQ ID :297:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :297:

GGAAACCAGC CCCTCACATC CTCCCTGAAC TTCCTGTCCC CACTCACACA 50
AGTGGTCCGG TGTCACCCTG CAGTTGGGTA TAGTCATAGG TACCATTGAT 100
20 GACGCCTTCT ACCTCGGCCA TGTAGGCCTT CCAGTCAACC TCTGTGTCTG 150
GAAGAAGACA AGATGATCTG GTTACTTTTG AGTCTAGAAC TTGTCTGCC 199

25 (2) INFORMATION FOR SEQ ID :298:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :298:

AAAAGATGAT AAATCCACCC TCNTGCTCTT AAAATCCCAT AAACGNTAGG 50
CTCTGGAGAA ACAAGTTGTT CTGTCGAGCC CTTGCCATCA ACACACTAAG 100
40 CAATCATAGT CCCCCAGAGC ACNAGATACT GCTAATGACC ATTANATNTT 150

163

GTATCATCAT GCTGCCTCCT GCATTGAAT T

181

(2) INFORMATION FOR SEQ ID :299:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :299:

15

AACATTGTTT ATTCATCCAG CAGTGTTGCT CAGCTCCTAC CTCTGTGCCA

50

GGGCAGCATT TTCATATCCA AGATCAATTC CCTTTT TAGC ACAGCCTGGG

100

GAGGGGGTCA TTGTTCTCCT CGTCCATCAG GGATCTCAGA GGCTCAGAGA

150

20

CTGCAAGCTG CTTGCCCAAG TCACACAGCT AGTGAAGACC AGAGCAGTTT

200

CATCTGGTTG TGA CTCTAGC TCAGTGCTCT TCCACTACTT ATATNCGCCT

250

25

TGGTGCCACC AAAAGTGCTC CCCAAAAGGA AGGAGAATGG GATTTTTTCC

300

GAGGCATGTA CATT

314

(2) INFORMATION FOR SEQ ID :300:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :300:

40

AAGAGTCCTG AAGGCATATC CAAGCCTGTT GTTCCTGCAG ACCTCATTAC

50

164

CACGCCAACA GAGAAGGCTG GACTGCTGCC CACATGCTGC TTCCAAAGGT 100
TTTAAGAACT GCCTAGAAAT CTCGTGTAGG CACGAAGGGC TTGAGCCAGA 150
5 AAGGAGAGAC AAGTGCAA 168

(2) INFORMATION FOR SEQ ID :301:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :301:

ACCCACATG CCCAGATGTC CACGNGCTTG CNATACGCCT CTTTGCAAAG 50
20 GACCTCAGGG GACAGGTACC TGGTGTGCCA GCGAAACCAA ACCATGCCTG 100
CTGGTTCCCC TGACCTCGAT AGCTAGGCCA AGTTTGCCAG CT 142

25 (2) INFORMATION FOR SEQ ID :302:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :302:

AGAATTCGTA ACTCATCCTA GAGTGGGCAC ATTTTAGACA TAGCAGGCGT 50
GATGACCAAC AAAGACTGAA GTTCCTATC TACGGAAAGG CATGACTGGG 100
40 AGGCCACAA GGACTCTCAT TGAGTTCTTA CTCGTTTCA GTCAAGACAA 150

165

TGCTTAGTTC AGATACTCAA AAATGTCTTC ACTCTGTCTT AAATTGG

197

(2) INFORMATION FOR SEQ ID :303:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :303:

15

AGAATTGCAA CTCATCCTAA GTGGGCACAT TTAGACATAG CAGGCATGAT

50

GACCAACAAA GATGAAGTTC CCTATCTACG AAAAGGCATG ACTGGGAGGC

100

CCACAAGACT TTCATCGAGT TCTTACTTCT TTCAATCAAG ACAATGCTTA

150

20

TTCAGATACT CAAAAACGTT TCACTCTGTC TTAAATGAAC AATTGAATTT

200

AAAAGTTTTT GAATAAATGA TGAAAATTTT TTAAC

236

25

(2) INFORMATION FOR SEQ ID :304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :304:

ATGTCATTCT CCTCATCCTC CGCATCTCCA CTGTCGTGCA CAAGGACCAC

50

CATGTTTCCT TTAGTTCCCA GCACACGGGG CTCTGCAGTA GTGAATGAAG

100

40

TCTAGCACAG CCACCGCCCC CATGCCAGG CTCAGGAGCA CACTGAGGTC

150

166

GTCCACCAAC ACACCGGGTA CGTCCACCGA GCCTCTCCAC TGCTCTGGCT 200

TTAGGCCTCC CGTACAAACT 220

5 (2) INFORMATION FOR SEQ ID :305:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :305:

AGAAGAAAGG ACACCATAC CATCCATATT GACATCGCAT TTCCATAGAA 50

20 ATGCCAAAGA AAGAAGGTCC TGGGGTTTTT TATAGAAGCT CAAAAAGNTC 100

AACCTTCGAT GCTATCCCCC AGCCCAATAC AAAATCAGAA AAAGC 145

(2) INFORMATION FOR SEQ ID :306:

25 (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :306:

35 AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50

TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG 100

40 NGNTGATATA AACAGATNNA 120

(2) INFORMATION FOR SEQ ID :307:

167

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :307:

10

AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50
TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG 100
NGNTGATATA AACAGATNNA 120

15

(2) INFORMATION FOR SEQ ID :308:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :308:

30

ACTGCACCCA CCCCAAGGCC ATGGCAGGGT ATGGAGATGT CATTATCAT 50
AAGATGGACA GATAAGCTGG ACCAATAATT AAGATTCCAG CAGAGGGTGA 100
GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAATGA TGGCAACGTC 150
TTGCCTTCCT GGGGACAGGG AGCCCTATTC AAANANAGTC ACATCTGAGG 200
AGCCGGGGGT TATAACATCA AGTCTGTCCT TGACCTCACA AAGCCAG 247

35

(2) INFORMATION FOR SEQ ID :309:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs

168

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :309:

AGGTAAGGTT GTCACGTGGA ACAACTGATA AAGGTCAGCT ATATATGTAG 50
10 AGCTATATAT GTGAGTCACA AGGTGTGTGA CATACGTGTA TACGTATAAT 100
ATGCGTT 107

15

(2) INFORMATION FOR SEQ ID :310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :310:

GGAAGACCTC GCTGGACATC CTGCAGGGCC ACATGGTGGC TCTGCTTGTG 50
ATTCTGGGGT CCACCCTCTC CAGTCAAGAG AACCCCCGTC GGGTTTAATG 100
30 TATCAGGAAA GAGA 114

(2) INFORMATION FOR SEQ ID :311:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

169

(xi) SEQUENCE DESCRIPTION: SEQ ID :311:

ATGGCAAATA GGAAGAAGCT CAGTATCCTC CTCCCACCAT AACCCCACTC 50
5 TCCACTGCCT CCTGGACCAT AGTTTCCTCC ACTATACGGT CCCCCCATGT 100
TCCTGCTACC ACCAAAGTTT CCACTCTTTA TCGAACCGTA TTAGAAGGTC 150
GCTGGTTATA ATTTCCAAAA TATGTAATTT CCACTTCCAA ATCCTTTATA 200
10 GTTGTCAATA CCACCTCCGT AGCCCCCACC CTGTTGC 237

(2) INFORMATION FOR SEQ ID :312:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :312:

TNNTCCACAA CAGNGGGACT ACTGAAGACT AGAGAACGCC TCTGTGNGAG 50
TGGTGCAGAC AAAGACCTCA CTAAAGTGNG CTTAACAGAG TACTAGAGGA 100
GAGAACTTGG CAATAGCAAG TACAGACAAC TATGTGAGAA ATACTGC 147

30

(2) INFORMATION FOR SEQ ID :313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :313:

170

CACAACAGNG GGACTACTGA AGACTAGAGA ACGCCTCTGT GNGAGTGGTG 50
CAGACAAAGA CCTCACTAAA GTGNGCTTAA CAGAGTACTA GAGGAGAGAA 100
5 CTTGGCAATA GCAAGTACAG ACAACTATGT GAGAAATACT GCTCCCAAAG 150
G 151

(2) INFORMATION FOR SEQ ID :314:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :314:

20

GAAGGTTGTA CGTGGACACT ATAAAGGTCA GCAAATTGGC AAAGTAGTCC 50
AGGTTTACAG GAAGAAATAT GTTATCTACA TCGAACGGGT GCAGCGGGAA 100
25 AAGGCTAATG GCACAACTGT CCACGTAGGC ATTCACCCCA GCAAGGTGGT 150
TATCACTAGG CTAAAACTGG ACAAAGACCG CAAAAGATC CTCGAACGGA 200
AAGCCAAATC TCGCCAAGTA GGAAAGGAAA AGGGCAAATA CAAGGAAGAA 250
30 ACCATTGAGA AGATGAGGAA TAAGTAATTN ATATANA 287

(2) INFORMATION FOR SEQ ID :315:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

171

(xi) SEQUENCE DESCRIPTION: SEQ ID :315:

5 GGAATCAAAC GNCTCTATAA TGAAGATAAT GTTCAGAAAA CGTGGGTTCT 50
GTGGTGACAC TGATTTATCA AGACAAGAGG GACATGCTTC CCCTTGTTCA 100
CCTTTGCAGC CTGTTTCTGT CATGTAGTTT CAACAAGTGC TACCTTGAGT 150
GTAAACTAAG GTAGACTACT CTGNGAATAA GAA 183

(2) INFORMATION FOR SEQ ID :316:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :316:

20 GGAATGAATC AAACGNCTCT ATAATGAAGA TAATGTTTCAG AAAACGTGGG 50
25 TTCTGTGCGT GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG 100
CCACCTTTGC AGCCTGTTTC TGTCATGTAG TTTCA 135

(2) INFORMATION FOR SEQ ID :317:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :317:

40 CGTTTGAAAT TCATCCCAAC TGTAGGCTGA GTGACCTGAA GTTGACAGAC 50

172

.. TGCCGAAGTC CAAAAGCTTC AGCATTTTCCT TAGTGTGAGG ATCTACTTCA 100
ATAATNNTGA TCCAAGGCTG AGACCTCAGA AACATAATGC TCTCCTTTCC 150
5 CTATNTTTTC TCGGGCTTGA TGGAGATACC TTTACTG 187

(2) INFORMATION FOR SEQ ID :318:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :318:

20 TCCCAGGAGA AGGAACTTTG AAATTCATCC CAACGTAGGC TGAGTGACCT 50
GAAGATTGAC AGACTGCCGA AGTCCAAAAG CTTGAGCATT TCCTTAGTGT 100
CAGGATCTAC TTCAATAATN NTGATCCAAG GCTGAGACCT CAGAAACATA 150
25 ATGCTCTCCT CCCTTNCTTT TCTGCGCTTG ATGGAGATAC CTTTCACTGT 200
GCCTCTCTGA ATCGTTTCAT CAGATGCTGA CGTAACCTGC TATTTGTTGN 250
AGCTTTCNGT TGNNTTAA 268

30

(2) INFORMATION FOR SEQ ID :319:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :319:

173

ACTGCACCCA CCCCAAGGCC ATGCAGGGTA TGGAGATGTC ATTTATTATA 50

AGATGAACAG ATAAGCTGGA CCAATAATTT ACAGATTCCA CAGAGGGTGA 100

5 GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAAT 138

(2) INFORMATION FOR SEQ ID :320:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :320:

AAATGATGAT AAATTCATCC TCTTCTGCTC TTAAAATTTT ATAAACCTCA 50

20

GGCTCTGGAG AAACAAGTTG TTCTGTTGGG CCCTTGCCAT CAACACACTT 100

GTAATCATAC TTCCCCCA 118

25 (2) INFORMATION FOR SEQ ID :321:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :321:

AGAACAGTTG AAGGTCTGAG GTGTTGAGAG GCAAATGGGG TCTCTGGGTG 50

GATCCTGGTC CTGTCAGCAG GCCTGGACTT GTTCAGGATG GACTGGTGGC 100

40

GTTATAAAGG GCAGATCAGG GTGCCTGTCC CTTGGCATGT CCCTTAAGAT 150

174

TTCCTTTTCC

160

(2) INFORMATION FOR SEQ ID :322:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :322:

15 AGGAGGGAGT TAATCCAAAC CACACAATGA AGTCTTCAAA CCACCNCCCC 50
AACAGGGCTG CTGATTGTTC CTTTCACTTT TGNGGTGACC TTGAGCTCCC 100
TTAAAAA AAAA AACTTGGAGA ATCACAACCTG GCAATGCACC GCAGTTCTCG 150
20 AACTACACAA GCATAGTCTG ACTAAGTCAC ATGTGTTTCC ATATCAACTT 200
GTTTGACAGG GCGACCTACT GCAAAGCAGG CTCAGTTACC CCACCAGTCA 250
25 ACCCCCTGGG AGTATAATNN TCTCCATANA A 281

(2) INFORMATION FOR SEQ ID :323:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :323:

40 GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC 50
ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTG 99

175

(2) INFORMATION FOR SEQ ID :324:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :324:

GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC 50
15 ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTGA 100
CACNNGTCCN NNGCNCNAGN TTACCATCCT TATGTGAATA CTNCAAGGGA 150
TTGCCCCGCGT TTTTAGG 167

20

(2) INFORMATION FOR SEQ ID :325:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :325:

TGATCCAACCT CTCCTGTGT GAAAAGAAGA ATGATGGCAG GAAGAACATA 50
35 AAGACTTTAA AACTCCTAGC CGGGGTTTGT CGGACTCTTT GNCAGTAGTG 100
ATTTAGCCAA CCAGGCAACA GAGATACGAT CTAATCTCCT CGCCCCCTCTT 150
TCGGGTCGCG 160

40

(2) INFORMATION FOR SEQ ID :326:

176

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :326:

10

GGAAGGGGTG TTGTTTGATA GACATTATCT GTGGCTGGGT CTTTCTGGCT 50

GATGAGAGAC ATGTAGATTA TGTGAAGCAA GTGGCTAGAA GATGAGAGAG 100

15

AACATGAGAG AGCAGAGTGC TCTC 124

(2) INFORMATION FOR SEQ ID :327:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :327:

30

AGCCTAGTTT GAACATCCTC ATCCCNGTGT TAGACCGGAT CCGATATACA 50

GAGTCTTAAG GAAATCGCAT CAACGTGCCT GAGCAGTCGG CTGTGACTCT 100

CGACAATGTA ACTCTGCAAA TCGATGGAGT CCTTTACCTG CCATCATGGA 150

35

CCCTTACAAG GCAAGCTACG ACGCGAGGAC CCTGATATGC CGTCACCCAG 200

CTAGCTCAAA CAACCACGAG ATCAGAGCTC AGCAAACCTCT CTCTGGACAA 250

AGT 253

40

(2) INFORMATION FOR SEQ ID :328:

177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :328:

10 GAACCTCTGG GCTCTCATCC TCTCCTATTG ACAGTGAAGC CCATGGCAAA 50
TAGAAGAAGC TCAGTATCGG CTCCTCCCAC CATAACCGCG TTNAATCGC 100
15 CTCCTGGACC ATAGTTTCCT CCACCATAAG TCCCCCATG CTCCTGCTAC 150
CACCGAAGTT CCCACTCCTG NGCGAACCGT AGTTAGAAGA TCGCTGTTAT 200

(2) INFORMATION FOR SEQ ID :329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :329:

30 TGACCTGATC ATCCTGAAAA ACTTTATGGG GGAGAAAGGT CAGCAGCTTC 50
TCTTTCTTTT NTCGAAAATN ATAAACTGC GTATTCTACT TTATATTTAA 100
35 TGTAAGGAAG AAAATATACA AGCCCATATT TACATCGTAT TTCTATTAAG 150
AGCAACAATA GTTCATATGT TCATGTTTGC TACTATCACA ATNCAACATA 200
TGAACACAGA TCAGCTCTAT ACCATGAATA CTGCTGGAAG TGATGGTTTA 250
40 GGATTACCAA CTCACTGCTG CCATGACCGA 280

178

(2) INFORMATION FOR SEQ ID :330:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :330:

CCTGAAAAAC TTTATGGGGG AGAAAGGTCA GCAGCTTCTC TTTCTTTTNT 50
15 CGAAAATNAT AAAACTGCGT ATTCTACTTT ATATTTAATG TAAGGAAGAA 100
AATATACAAG CCCATATTTA CATCGTATTT CTATTAAGAG CAACAATAGT 150
TCATATGTTC ATGTTTGCTA CTATCACAAT NCAACATATG AACACAGATC 200
20 AGCTCTATAC CATGAATACT GCTGGAAGTG ATGGTTTAGG ATTACCAACT 250
CACTGCTGCC ATGACCGA 268

25 (2) INFORMATION FOR SEQ ID :331:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :331:

TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT 50
AGAGTTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN 100
40 TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC 150

179

TACCATATGC CCTTAAAAAT

170

(2) INFORMATION FOR SEQ ID :332:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :332:

15

TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT

50

AGAGTTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN

100

TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC

150

20

TACCATATGC CCTTAAAAAT NNGGNNNNNG NNNNGGNTGA ANGGTTCTGT

200

GTTCCAAAAA TNTAAGATTT GTT

223

25

(2) INFORMATION FOR SEQ ID :333:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :333:

AGACAATTGG CGGCATCCTC GTAGGCTTCA CTAAGTCCCA CAAGTTCTTC

50

TGGTTTCATT TCGGTTATTT TTTGCAGCCA ATTCTCTCCA TGTTTGGCAG

100

40

TCACAAGGCT CATGTGCTTC ACCAAGGCAC TC

132

180

(2) INFORMATION FOR SEQ ID :334:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :334:

AAGTTGTTCA TGGNAGGCAT TTATCCTNTC AATAATNCAA ACGAGGCTTC 50
15 TGGAATAACC AGTGCCCCAT TCCATCAGAG TCTTTGCGCG ACTAAAGCCT 100
CCATNTTTGC CAATTTCAAT TGTTTGGGAT TCTAGCACTC CTTACCNGCA 150
GTAATGCCCT TGCTGCAGAC AACAACACCT GGACTGNGAG ATGGACCAAT 200
20 TCTCAATGGC AATCCAGGGA AAGAGTGATC CTTCT 235

(2) INFORMATION FOR SEQ ID :335:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :335:

35 ATGCCCGCAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC 50
ATTGAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTTC AAGTTTCA 100
CACTGGTAAC CTGTGTATGG TGACTGAGGT GCTAACCTAG GAAGAATTGG 150
40 GNGATCACCA ACAGGAGAG 169

181

(2) INFORMATION FOR SEQ ID :336:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :336:

ATGCCCCGCAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC 50
15 ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTTCA TCAAGTTCGA 100
CACTGGTAAC CTGTGTATGG TGA CTGAGGT GCTAACCTAG GAAGAATTGG 150
GNGATCACCA ACAGGAGAGG CACNCTGNAN TCTTTTGGCN NNG 193

20

(2) INFORMATION FOR SEQ ID :337:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :337:

CAAAAGTCAT CCACAAGTTC TTTGTCTAGG ACTTCTAGCT GCTCAGACCC 50
35 TCAGGGTCTT TGGATTGTTA CCAAAGTCTG TCAAACAGAC CAGTAGTTTA 100
ATACCTGTAC AGAAAAATGT TTCTATTATG CTTCTAGTAT CTAGAAATTG 150
CTTGCTACAG CATGGAGGTG GTTCTGCCTT TCCCTGGCTC CTCACACTCT 200
40 CATCTGCAGG ATTCCCAGCT TTGCTCAGTC TTCATGCCCA CCAGAGGCAA 250

182

AAAGGCAAAC TAAAACTGTC ATGCAGTGGT AGGTTTGAAA TNAGCTGCTG 300
CATCATG 307

5 (2) INFORMATION FOR SEQ ID :338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :338:

AAAAGTCATC CACAAGTTCT TTGTCTAGGA CTTCTAGCTG CTCAGACCCT 50
CAGGGTCTTT GGATTGTTAC CAAAGTCTGT CAAACAGACC AGTAGTTTAA 100
20 TACCTGTACA GAAAAATGTT TCTATTATGC TTCTAGTATC TAGAAATTGC 150
TTGCTACAGC ATGGAGGTGG TTCTGCCTTT CCCTGGCTCC TCACACTCTC 200
25 ATCTGCAGGA TTCCCAGCTT TGCTCAGTCT TCATGCCCAC CAGAGGCAAA 250
AAGGCAAAC TAAAACTGTCA TGCAGTGGTA GGTTTGAAAT NAGCTGCTGC 300
ATCAT 305

30

(2) INFORMATION FOR SEQ ID :339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :339:

183

AATATAAAGA GGAAATGGCT CNTCACCTTC ATAATACCAA GACCTGCTCA 50

ATTTAAGATG GCCCTTGACA TTGAAATCGT ACCTACAGAA AGCTTGNAAG 100

5 G 101

(2) INFORMATION FOR SEQ ID :340:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :340:

GTGCGAGGAG AAAAAAGTCG TCACGTCATG CGAGTGGCGA GGGGGCGTGG 50

20

AGAGTAGCAG TAGAGCAACA AAGTACATAT AGGACAGTGC AGCGAGGACA 100

AGGACTTCCC GCA 113

25

(2) INFORMATION FOR SEQ ID :341:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :341:

ACACAAATAA CTACATNTAC GCAATATAAT NTTTAAAAAT CCAAAGCAAT 50

ATAAAAGAGC AGAGCTAGGA CTGAACAGAA CATTTTGGTG TATAACCGGC 100

40

AGCTCAAAAT CGCCAGCTGA TTGGAGTAAA ACTGATTCTA AGCGTATTAA 150

184

ATACGATTGA TTGTTTCCAT CACTAAGGGT GCCTATGAGT TTCTGAACCA 200

TTTCTAGGG 209

5 (2) INFORMATION FOR SEQ ID :342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :342:

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50

TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA 100

20 GCTTTTAATC TTCATTTTTN NNTTTTGTNA TGGTAGGCTG AGATGCTTTT 150

AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT 200

25 TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC 250

TA 252

(2) INFORMATION FOR SEQ ID :343:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :343:

40

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50

185

TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA 100
GCTTTTAATC TTCATTTTNN NNTTTTGTNA TGGTAGGCTG AGATGCTTTT 150
5 AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT 200
TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC 250
TACAAAAC 258

10

(2) INFORMATION FOR SEQ ID :344:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :344:

GAAGGAACCA GTGACCAGTC ATCCCCAGAG ATAGATGAAG ACCGGATCCC 50
25 CAACCCACAT TCAAGTCCAC TTTGCAATGT CTCCACGGCA ACGGAAGAAG 100
ATGACAAGGA TCACACCCAC AATGAAAGAG CTCCAGATGA TGGTTGAACA 150
TCACCTGGGG CAACAGCAGC AAGGAGAGGA ACCTGAGGGG CCGCTGAGAG 200
30 CACAGGACCC AGGAGTCCGC CCACCTG 227

(2) INFORMATION FOR SEQ ID :345:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

186

(xi) SEQUENCE DESCRIPTION: SEQ ID :345:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG 50
 5 TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC 100
 CTGGCACACT ACTAAACTGT AAATGTTTTT AAATCTGAAT CTGTAGAATT 150
 CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCA 188

10

(2) INFORMATION FOR SEQ ID :346:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 262 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :346:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG 50
 25 TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC 100
 CTGGCACACT ACTAAACTGT AAATGTTTTT AAATCTGAAT CTGTAGAATT 150
 CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCATG NCTCTGGATT 200
 30 NNCTNNNAGG TTTTAAGATG GAGCATCTGN GNATGTCAGC CCGTCCTATC 250
 TAGAAGTGNA AA 262

35

(2) INFORMATION FOR SEQ ID :347:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :347:

5 CTCTGTTTTT CAAACGCCCA TGTGTGCTAT ACTACAAC TCCTCGAGTC 50
TGATCAATTT GCAGTAGACC ATTTTAGTTC TTACGACGTT AATAACAAAC 100
ACTTCAACAT CANTGCTCCA ATCTGAAGTT CTTGTTGCAT TGTTAAAAGA 150
10 AATNTCTAA 159

(2) INFORMATION FOR SEQ ID :348:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID :348:

25 TCGCAGGAGA AGGAAGCTGC ATGCACTTGA AAGGCATGGC CTGTCTCCTC 50
ACTGAGTGCA AGGTCCATCG ACCAAAGCCC TGTTCTGATC AATAACATCT 100
ACAATCGCAC CAATTTTCCG GCATGAGGTC CAAAGGAGAC ATAGGCCACC 150
30 CGGCCAACCT CCACGAAGCG CCTGAACACC ATGCGCTTCC CGGGACCCTC 200
TGGGAGCCGT TCGCNCCTCA GCTTCCCAGC GAGGTGGAGG TCGAGCGGCA 250
TGGNCGACGC CCCGGAGCCC ACAACAGTAA GAC 283
35

(2) INFORMATION FOR SEQ ID :349:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :349:

5 CAGAAAGGAG GCATTGAGCA AAAACTAGGA AAATCTGAAT AAACNGTGG 50
CCTCGCTTGG TTAATATATT TANACTGGTG ACTCATTTTA AAACTTTCCC 100
GGGCGCGATG GCTCATGTCT GCAATCCCAG CACTTGNGAG GCTGAGCGGG 150
10 TGGATCACCC AGGTCAGGA 169

(2) INFORMATION FOR SEQ ID :350:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :350:

25 GAAGNAACCA GTACCAGTCA TCCCCAGAGA TAGATGAAGA CCGGATCCCC 50
AACCACANT TAAGTCCACT TTGCAATGTC TCCACGGCAA CGAAGAAGAT 100
GACAAGGATC ACACCCACAA TGAAAGAGCT CCAGATGATG GNGAACATCA 150
30 CTTGGCAACA NCACAGGAAG GGACC 175

(2) INFORMATION FOR SEQ ID :351:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

189

(xi) SEQUENCE DESCRIPTION: SEQ ID :351:

AAATAAAAA TAAGNACCCA ACCAATGCTA CAGATAATAA GAGCTCAGTA 50
5 AATGTTGATT GAATCACTAA CAAAGATAAA AGCAGACGAC ACAGTACCTG 100
GCACACTACT AACTGTAAAT GTTTTAAAT TGAATCTGTA AAATTTGTAA 150
GGTTTTATGA ATATAATATT ATTAAC TATT ATGTCTCTGA ATTTTNNNN 200
10 NAGGCT 206

(2) INFORMATION FOR SEQ ID :352:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :352:

25 AGACATACTG TAGTGTCTAA ATAATATTG TCNGAAGATA ACAATTATGG 50
GACTTTAAAG CCGACAGTGA AATTAT 76

(2) INFORMATION FOR SEQ ID :353:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :353:

40 ACATTTGGCC CTCAGACTGT AATTCCATA CTA CTNTGAC TGATACTAGA 50

190

100 TGACCTGGCT GCCTAGGGGC TGTGCTGGTC TGATTTTTTG TGAGACAAA
150 ACCACTCTAA ACCTCCTGGT GCACTGAGGC TGTACACACC GNCAGAACAG
5 GGCCTGCGT TTAAAAGTTT CTGACCAAGT GGTGACAACA GAGGNCAAC 200
GTAAGGCTGT CTGGATAAGT TGAACCTNGC TGANCGGTAG CACCA 245

(2) INFORMATION FOR SEQ ID :354:

10

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :354:

20

GGAATCTGTG CCACACAGCT GCACACGACT ACTGGCCAAA GGACAGCCTC 50
AGAACATCAT GAGCTGGCGT GACCTCATGA TGNNCCTCAN TGCTGTGGGG 100
25 CTTCTGCTNG AGGCCAGCAG AGGCTCGTAT GACTACCTGT NAGACCTGCT 150
CTTTGGGTTG AGACTTTTCA GNGACAACT 179

(2) INFORMATION FOR SEQ ID :355:

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :355:

40

AAGGAACGNA TGACTTTCCA TCCCTTGAAC CAAGGCATGT TAGCACTTGC 50

191

TCCAGCATGT TGTCAACCATT TCAACAGAAA TCGCACAAAT GCTACTGTGC 100

AAGGTGCAGC CAATTTTNTT GTAAGTGTGA TTTCTTACG 139

5 (2) INFORMATION FOR SEQ ID :356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :356:

TCCAGGAGAA GGAAACTTC CACTTATAAC TGTNTCAGCC TGACTATAAT 50

GAAGAGACTA GCAACACCTC CTGAACACAA GCCTANTGAG CCCAGTCTTT 100

20

(2) INFORMATION FOR SEQ ID :357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :357:

AGAAGGAAAC ACCAAAGAAA CATCCAAGCA ATAAAGTGGG AACTAACCA 50

35 AGATTTGGAC ATTGGAATGT TTAGTGTAT TCTTAAGAA ACAACTACAA 100

AAAGAAAATG TCAACAAATT TTCCTAGCT AACTGAG 137

(2) INFORMATION FOR SEQ ID :358:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

192

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :358:

10	AAGGAACAAG TGGGTCATTC TACTAAGGC TGCCTGTCAC TGCAGTCTTG	50
	ATCAGCTTGT CAATTTGATA CTTCAGCTTT TGGTCCAAGG GACGAAGCTT	100
	TTCCAAAACC GTTCGAATCT CTACCAGTCT CAAAACTGCA TCATGTCCCT	150
15	GAAGAGATCC TCCTGAGGCT TTGTCCAGAA TGAGGTGGGT CAAATNNANG	200
	GGNACATGAG CAGCAGCTGN TCTTTAAC	228

(2) INFORMATION FOR SEQ ID :359:

20

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 248 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :359:

30

	CAGGAGCAAG GAGGCCATTT TGCTGAGCTC TCACAGCTGC TAGAGATGCT	50
	CAATGACTCC CAATACAACC CAAAGAGACA AACGCTTGTT TTTTCTGCCA	100
35	CACTCACCCCT GGTGCATCAG CTCCTGCTCG AATCCTTCAT AAGAAGCACA	150
	CCAAGAAAAT GAATAAAACA GCCAACTCG ACCTTCTTAT GCAGAAAATT	200
40	GGCATGAGGG GCAAGCCCAA GGTCATTGAC CTCACAAGGA ATGAGGCC	248

(2) INFORMATION FOR SEQ ID :360:

193

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :360:

AGGCACCTGT GGAGCCATCC TCCTTGTTTT AATCGTCCTG CTGCTGCTGC 50
CGTTCCGTGT CGCGTCGCCC ACATGACCCT GAGGTCGCAA TGATGAGTCC 100
TCTCTGGTCA GACACCGCTG GAAATGAATA CCAGGCCTGA CCTCAAGCAA 150
CCATGAACTA GCTATTAAGA AATACANNGG NAGGGCGGCA GCCGGATCGT 200
GNNGGCGTTT NTCTGNGCCG CCCGTCTCAA TCTNTGTTCT GCTTCCAGAT 250
GCC 253

(2) INFORMATION FOR SEQ ID :361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :361:

GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG 50
GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT 100
CTAAACNNGC TNGGCNATGT CGTAGTTNCT TGTCAGTNGA TCGGTAGAGA 150
TAAT 154

194

(2) INFORMATION FOR SEQ ID :362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :362:

GAGAACCACG	GGCTCCATCC	TGGCCTCCTG	TNCACCTTCG	AACAGATGCG	50
GATTAGCAAG	CAGGAGCACA	CGAATCAAGC	CCCTCCAGCC	ACCAAATTTT	100
CTAAACNGGC	TNGGCNATGT	CGTAGTTNGT	TGTCAGTNGA	TCGGTAGAGA	150
TAATCCTGNC	CACGCCCT				168

20

(2) INFORMATION FOR SEQ ID :363:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :363:

AAGGGATAAA	AGGAAGCTTT	GNCACCACTC	TACCATCAAA	NNGGAATTGA	50
ACATTCCCAT	TAAGGCAGTA	AAACAAAAGC	CAATAGCAAA	CATGNATTTT	100
ATTCAACCAT	TGATAGATCT	CTGCCGTTAT	TCTTCAGTTT	CTCTTCTCGT	150
CTCTCTATTT	NTTTCTCTGG	TTGTCGACCA	GCTGACTNTG	NCATCGTT	198

40

(2) INFORMATION FOR SEQ ID :364:

195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :364:

10

TTATACAAGT CAAACTTGGA AGGTCATAGT AAGCATACCT ATGCTGAGAG 50

AAAAGCATCA AATCCTCCGC GACACATCTA GTTCATCGTA ACAAAGCAAC 100

15

TCGTACACTT TCAAGTTTAA A 121

(2) INFORMATION FOR SEQ ID :365:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :365:

30

GGTAAGTTGT ATTTGGGCCA GAATTTTAAA GAGCACTATT TCGACATTAA 50

AATGTATTCT TCTCGTATTA ATGCCTACAT CTCAGAGTT TTCAATGCTT 100

TCTAAAAGTT TCCTCTTTGG AAAGAAGAAA TCTGAAAGAC CTATCATGCC 150

35

GTTCTTCCTG GCGTCTATAT TTCCTTTAGA GAGGCAAGGT AGGATTCCTG 200

CTCCAAGGGA G 211

(2) INFORMATION FOR SEQ ID :366:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs

196

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :366:

CGGCTACAGC ATCACATCCA CTAAATGCAC AGTTGTTGAA GTCACGCCCT 50
10 GCCAGACCTC TACTACCACA TTGTTCCCTC CGGTGACCAG TTTGTCCGTC 100
ACTGTCAGGA GAATGNCCCG TGTCGAATCA TCGATCTCCA TCCGAGCCAA 150
15 AAGTTTTCCA TATGCTGAAA TTACTGAATT GCCCTCGTTT ATAGTATATG 200
ATACAGTGGC CTTGTTGGA GGCAGATATC AAGCATGGGG ATAAGCAGTT 250
TTCTGGTCCT TAAGGGCTCT CAGCAAATCT CCGTG 285

20

(2) INFORMATION FOR SEQ ID :367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :367:

GACACTGAGG CAGCTACTGA GAAGGGCAGA ACATGTCTCA ATCCATAGAG 50
35 GTCTTGGCAG GCGAACCCAG AGAGACTTGC AGTACGTGAG AAGATGGAGA 100
ACCAAATAAA AGGACTGGAG TCCAGTTCAA ACAAGGAGGG AGTGGTAGT 149

40

(2) INFORMATION FOR SEQ ID :368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs

197

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :368:

GGTCCCGCT CTCACAGCCA TTGCAGTACA TGAGCTCCAT AGAGACAGCG 50
10 CCGGGGCAAG TGAGAGCCGG ACGAGCACTG GCGACTTGTG CCTCGCTGAG 100
GCAATACTAT AATANGCAAG GAACTTTTGA GGCCGAG 137

15

(2) INFORMATION FOR SEQ ID :369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :369:

GCCATCATAA GTTCAAAAGA AAAGAGAAAG TGTTATTTTT CTGTTAGTGA 50
CATGTAGTCC CTTTGTCTA GTAGGAAAAA AGGTGCCTAG AGGTAGTATA 100
30 TAGAGTAAAT ATTGTTCTT TGCCTACTCG TGCTTCCAAT GATTAAGGAA 150
ATGTTAAACA NNNGTNAAAG TCTGTTTTGT CAATGCGGGA GT 192

35

(2) INFORMATION FOR SEQ ID :370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :370:

5 GAGACTTAAG TAAAACGGCT GCAGGCCAGA TCGCCCCACC AGCTCAGAGA 50
CCACCTTTAT CCATGCTTTG AAGTAGGACT CCTTCCGTCT TCAAAATNTT 100
GAAGACCCTA ACANGCTTTT ATGATGGGGG TCATATCTAT GGTCACGNAT 150
10 ATAGTAGAAA CCAAAGAAT GTAAGTATTT GTNNATGATT TAAAAAT 197

(2) INFORMATION FOR SEQ ID :371:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :371:

GCATCTGNCA GCTGCTGCAG GCTGACAGCC TCCAGACCTG GACAGAATTC 50
25 ATACACTCCC GGAGCTGAAA AAACCGAACA TAAGGGAGTG CACAAGAGCC 100
GGGCTTTGGA GAGG 114

30 (2) INFORMATION FOR SEQ ID :372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :372:

CTTTCTCTAC TCCATCCATT ATCTCCGGGA TTCCTCCACA TTCCCTTCAG 50

199

CTCCTAGTTG TTCCACCTTG GCTAACAATT TACCAATCTT TTTTCTATG 100

AACACGTTCT GCCTTTGCTG CTA CTCTTC 127

5 (2) INFORMATION FOR SEQ ID :373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :373:

AAGCGCTCAA TTCGCATCCA CAATGCAACC ACGAACTGAT TTTCTCTTTC 50

TTTTTCAGTT CTCCTTGGTC TGTAACAGGA ATGCCCCTTA CTCAGTAGCA 100

20 GGCGGACACG GCCATGGGTC AAGACACCCT GCTTCATGGG GAAACCTTGT 150

TTGTCGTTCC CACCACTGAT TCGGACCACA TAACCTTATN NNATCCCGAG 200

25 CGTTAGCAGC AACTTTTGTG GCCATACGCT TCTCATAGAA AGTACGAAGT 250

TTGGCAT 257

(2) INFORMATION FOR SEQ ID :374:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :374:

40

GCATCATCAT TGACATCCCT ATCAATGTCT ACGCTGCTGG CAGAGGACTG 50

200

NCCATTTGGA GCTGAGATGT GTAAGCTGGT GCCTTTAATA CAGAAAGCCT 100
CCGTGGGAAT CACTGTCTGA GTCTTGTC TAGTATTGAC AGATATAGCT 150
5 TTGTTCTTGG AGTAGAATTA AGGAATTGCG 180

(2) INFORMATION FOR SEQ ID :375:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :375:

GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT 50
20 TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGNC 100
TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT 150
25 TCAACCAAAA TNGATATCAG CAATGTAAAA ATCCCAAAC ATCTTACTGA 200
TGCTTACTTC AAGAAGAAGA AGCTGCGGAA GCCCAGACAC CAGGAAGGTG 250
AGATCTTCGA CACAGAAAAA GAGAAATATG AGATTACGGA GCAGCCAAGA 300
30 TTGATCAGAA AGCTGTGGAC TTA 323

(2) INFORMATION FOR SEQ ID :376:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

201

(xi) SEQUENCE DESCRIPTION: SEQ ID :376:

	GGGGAATCCC ACCTCACCCA TTGNGGTGAA ATGCTTTTTT CTAAGAGGTG	50
5	AAATCACTCG CTGGTGTTTA TTTCGGCACA ACCAGAAAAT AGTGNGGGAT	100
	ATTGAATTAT GGGAGGCTCT GACTGTCTCG NGTGCAGCTT ACATTCACAG	150
	ATGGGGGGTA GTTTTTATAT TCTATAAGCG AGCATATTAA ANGCAATATG	200
10	AGTCAGTCCT GCATTTATGT CTT	223

(2) INFORMATION FOR SEQ ID :377:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 122 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :377:

25	GGCTCAGGAT CCGGCATCCT TTATGCCTCC ACAGCACCTT GCTCTTTCCC	50
	CAGCCAATCA CTTTAGATGC TGAATCGATT TTAAACANAT GTTTTGTCAT	100
	ATGGCTAATC AAGAGCCAGG TA	122
30		

(2) INFORMATION FOR SEQ ID :378:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 195 base pairs
35	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :378:

202

GGCAGTGCGT GCTTCATCCC TTTATGAAGA ACAGAAAATT ATGACTACTC 50

TACAAGGTGG ATAATACTTC GGTACCTTGC TTGCCACAGC CCTGTTCTC 100

5 AAAGCTGAAT TGATAAATTT CTCTTTGACT TCCAAGACCT AGCAGTTATA 150

AGGCGCCTTG AATAAAGTTT GTGCCTGAAA ATGTGGAGCA ATGCT 195

(2) INFORMATION FOR SEQ ID :379:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :379:

20

GTAGCCCTGA GGTCATCCTG CAAAGNGCGT ATCAAAAAAN ACGAAGTTAG 50

GGTGACAAAG TTTGACAGTG ATGTTTACAA GTCAAACCTTG GAAGGTTATA 100

25 GTAAGCATAC CTANGCTGAG AGAAAAGCAT CAAANCTNNG GNACATANTN 150

GGTTTNTNGN AACAAAGCAA CTTGTAATTT AAGNTTAAAC NGAGCATCAT 200

ATANNNNNGG 210

30

(2) INFORMATION FOR SEQ ID :380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :380:

203

CTGGCTCACC TGGACAACCT CAAGGGCACC TTTGCCACAC TGAGTGAGCT 50
GCACTGTGAC AAGCTGCACG TGGATCCTGA GAACTTCAGG CTCCTGGGCA 100
5 ACGTGCTGGT CTGTGTGCTG GCCCATCACT TTGGCAAAGA ATTCACCCCA 150
CCGTGCAGGC TGCCTATCAG AAAGTGGTGG CTGGTGTGGC TAATGCCCTG 200
GCCCACAAGT ATCACTAAGC TCGCTTTCTT GCTGTTCA 238

10

(2) INFORMATION FOR SEQ ID :381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :381:

GTCCTATGGC ATGAATGTTT GCAACCAACC CAGGAAAAGC CTAAAGGAA 50
25 ATAGCTGTTT ACATAGGAGA CCGTGACAAT GCTGTACGCA ATGCTGCACT 100
CAACACCAAG CAACGATGCA CAATGTACAT GAGGATCAGG TGTTCAAAC 150
GATTGGAAAT CTTTTTGAAA AGGATATGAG CATGCTCGAG GAGAGGATTA 200
30 AGCGTCAGCA AAGAGACCCT CTCTGCACCA ATAAACAGG TGGAAGAAAA 250
CCTAGCNCGC ACAGAACATA AGCTC 275

35

(2) INFORMATION FOR SEQ ID :382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :382:

5 AAGCAGAGTA CGCACGTCAG GCCCTTCCAC GCCCACCCTCA ACACCTTTAAA 50
CNTACTGGGC GATGGGGCCG TTTNGCTGGC AGTTCAGAT AAAACA 96

(2) INFORMATION FOR SEQ ID :383:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :383:

20 GGACTTGATG GCTTCTTTCA AAGTCATAGA CTTGTGGTAA ACTTCTTGCA 50
AGGAGCTCTG GGCACCCTCT GAAGCAGAGC CAATTGCTCG AGCATCACAC 100
TGTACAAAGG TCCAGATGGG TTCATATGAA ACAGCTGGAG TCCTTTTCAT 150
25 CAATNCNAAT NGANNGGTTA CTCCAAAGGG ACGAGACATG CACCTG 196

(2) INFORMATION FOR SEQ ID :384:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :384:

40 AAGGAGGCCT TTGAGTCCCA TCCTCTGCCA CGCAGAGAGG CAGGCCTGGC 50
ATTTCAGCCT CACTTTGTGT AGGTCACTTT TCGGTCTGTG TTGTAGCTCA 100

205

CCAACCAACA GTCAAACCCC AGCGTGGTAG CACGAGGTCC AGAACCTCTG 150

CTTAGTGGGC CCGTATAATA AACGCAACCT GACCCAATTN NGGTTTCTTT 200

5 CCCCAT 206

(2) INFORMATION FOR SEQ ID :385:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :385:

GAATGCTTGG GATCATCCAG GTGNCTCTAT TTATAGGCAC CTGTGTTTAC 50

20

CAGCAGTCTC TCTATTAGAA TGCTTGGTGT GCCAATGTTT CTTGAATTAG 100

AAGCCTGGGG NCACCTAGGT GTTTCTATTA TAAA 134

25 (2) INFORMATION FOR SEQ ID :386:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :386:

CAAGGCCTTC CTGCACTGGT ACACGGCGAG GGCATGGACG AGAGGAGTTC 50

ACCGAGGCCG AGAGCAACAT GAACGACCTG GTGTCCGAGT ACCAGCAGTA 100

40

CCAGGACGCC ACGCCGACGA ACAAGGGGAG TTCNGAGGAG GAGGAGGCCA 150

206

GGACGAGGCG T

161

(2) INFORMATION FOR SEQ ID :387:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 170 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :387:

15	GGTGAGCCTC CGCCATCCAG CAAAC TGTGC TGAC CGCAGCTGTG	50
	CCGTGGCACG ATGGCGAGGA AGCCAGCCCC AAGGA CAC TGAAAACACA	100
	ACCAGTCAAT GCCGTGTGGT TTTGTTTGAA TATAAATNGC TGAAAGTGTT	150
20	GTTTTTTNAG GCAGTAATNT	170

(2) INFORMATION FOR SEQ ID :388:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :388:

35	TCCATCTGAC ATCGCATTTT CATAGAAATG GCCAAAGAAA GAAGGTCCTG	50
	GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA	100
	GCCCAATACA AAATACACAG AAAAAGCAAT TATTA AAAAC GGCTTCGGTT	150
40	TCTTTTTTCT CTTTAATNNC CTACAATNGC TTTACATATT CGTGTGCAGC	200

207

ACCTACTTCT TTATGCCGTG AACTGAAATC TAAGATTTC AACTGAAATC 250

(2) INFORMATION FOR SEQ ID :389:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :389:

15 GCCATCTCCC CGCCACCCNC TCGTCCCCTT CTTNTCNNGC CACCCTTCCT 50
CNCTCNTCCG TTTTNGCTCC ACTCCACTCC TCCNTTTTNA GTACCCTCCT 100
CNTTTATNTA GAGTTACTGA GAGCCGACCT GACGTCTCCA ACATNCCGTN 150
20 TCTTATATCT CATCNCGGTT NTNGANGAAT GNAGTNAGGG TTCCGGGAG 200
AGACCNAACT TGCTCTAGCC CTTTCCAGCC GCTGTTGTTA AACTGACCTC 250
25 GTAGGGCNTG AGGGAGGT 268

(2) INFORMATION FOR SEQ ID :390:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :390:

40 GTCAGAGGCA GCCCATCCAG CACGTGCTAG GTGTTCCCAT ACGCACAGGA 50
GAGGCGAGCT AGCCAGCCAA GGCGGGCAGG CGGGGAGGCC CTCTAGCTGT 100

208

TTGCCTCACC TGTGGGGCCC CAGCAGGGAG GAGTCACCAG CCTAGAGGGG 150

CCAGGTATAC ACCTTANAGA GGATGAC 177

5 (2) INFORMATION FOR SEQ ID :391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :391:

GCTCCACTTC CCACATAANA CNAGACCTCT CACAAAAGAG TTCACTGATA 50

TGTGAATGCA GCTTTCTCCC CATGGTAGCC AGGACAGGGT GCACATTAAG 100

20 GCAACCCCAA AAACACCTCT TNCTGNCTGC CTCTGCAA 139

(2) INFORMATION FOR SEQ ID :392:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :392:

35 GAGGAGCTGC CCTCAAGGTC GTGCGTCTGA AGCCTACAAG AAAGTTTGCC 50

TATCTGGGGC GCCTGGCTCA CGAGGTGGC TGGAAGTACC AGGCAGTGAC 100

AGCCACCCTG GAGGAGAAGA GGAAAGAGAA AGCCAAGATC CACTACCGGA 150

40 AGAAGAAGCA GCTCATGAGG CTACGGAAAC AGGCCGAGAA GAACGCGGAG 200

209

AAGAAAATTG ACAAATAATA GAGGTCCTCA AGCCCACGGA CTCCTGGTCT 250

GAGCCCAAT 259

5 (2) INFORMATION FOR SEQ ID :393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :393:

AAAGATCATC AGTTTGGAAG GTACTGGTCC AATTTATCTA GGAAGTATCT 50

CTTGAGTTT CAGAAATGCT AGCTTGGACA ACTGAAAAGT CACATCACAG 100

20 CTGGCATTCT GGGGGCTACC AAAACACCCC TCNNGGAGTA GAAGCTGCTG 150

GAAGGCAGGC CTGAGCCATT CACCACGGAC AGGAAGAGC 189

25 (2) INFORMATION FOR SEQ ID :394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :394:

AGAAGGGGAG GTCGAAGAAA TGTGGCTGAT CATAAGAAAG GAGCAAAGAA 50

AGCTAGAATT GAAGAANNNN GAAAGAAACA GAGGACAAAA AAACAGA 97

40

(2) INFORMATION FOR SEQ ID :395:

210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :395:

10 AAGAGGGGCT AAGACCCAAG TCATCCTCCA CTTTCGTTTT GTTATATTTT 50
GCTTAGAATT GCCTCTTCTT CTCCACTTCA GAACTGCCTC AAAATTGACC 100
15 CCCTTGACTG ATTTATTGTC GTCAAAGCA TGTCCTCTA TCTTTTNNNN 150
TCACACGATC CGCTGCCTTT CTACATCTGA GAATCTTGTC AAGCATGGAT 200
AAACTTGNTT TTATGTTGCA TATTTTNACG GCTTCAACTT GAGT 244

(2) INFORMATION FOR SEQ ID :396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :396:

TAATATCGCC ATGTAATGGT ATACATTGTA AGGCTTATGT CACTAAAGAT 50
35 TTTTATTCTG ATCTTTCCAT AATAAAGGTC ATATGATACT GTATAGACAA 100
GCTTTGCAGT GAAGTATAGT AGCAATAATT TTCGTACCTG ATCAAGTTTA 150
TTGCAGCCTT TCTTTTCCGT TTCTTTTNTG AAGGG 185

(2) INFORMATION FOR SEQ ID :397:

211

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :397:

GGACACATCC ACCCAGTGAA CTGGACTGTG GCCATGACCC AGGGTATCAG 50
CTCCAAACTC TGCCAGGGCT GAGAGACACA TGAAGGAAGA TGATGGGAGG 100
AAAAGCCCAG GAGAAGTCCA CCAGGGACCA GCCCAGCCTG TATACTTGCC 150
ACTTACCACC AGGACTCCTT GNTCTGCTCT GGCAAGAGAC TCTTGTCTGA 200
ACACTGCTTA TCTGACCC 218

(2) INFORMATION FOR SEQ ID :398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :398:

GGAAGCAAAA AAACAAACT AAGCTCGAAT TTGCTTCCAA ACCTGTAGAT 50
TGCATCTAAC CANGTGTCCC TATGCACCTC AGAGTACTGG AATACGAACC 100
CAGCGAGACC TTGTCCCCTC CCATTTTGCT GNACTTTTGT TGGTGAAAAT 150
GAGAATGAGT TNATCCCTAC NTACTTAGTT TAATGCATTT GACCCCAGAA 200
AACCCAGTA CCTTTNNACA ATGACCCAAC CANTACCTAC CATCGGCCAG 250

212

(2) INFORMATION FOR SEQ ID :399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :399:

	TCACCTTGATT CATCCGTCGC GGGATTTGGG AGCACTAGCA ACATAATCAA	50
15	CACACTCCTA CAATCTTAGG CTTACATGT GCTGATGATG ATGAAACCAA	100
	CTCTGCCCCA ATCATCTCCC CTTCTNNTAG GGTCTTACTA CATATCGCAA	150
	CAGAAGATAA TATTGAGGTG AAGAGGGTAA CATGAAGTTT GGCCTACCC	200
20	TGAAGAACTG TAGGCATCTC TTGGAATGTG CTAAGGAACT TGATGTCCAA	250
	ATAATGAGAT TAAATTTATG TTTCGAGT	278

(2) INFORMATION FOR SEQ ID :400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :400:

	GGCCAAACTC ACAGGAGCCT AGGCACAGAG CACTGAACAC TGGCTCTGCA	50
	GCGGGAAGGA ATTAGAGCCT TCTGCTTTTG CACCTGCTTT GAGTTAGGAA	100
40	GCAAGCTCTC TTCCTTGCCA GACTTCCCTT TGGGGCAGGA CACTTTTTTA	150

213

TACNCTGAGG CAAGGCAAAC AGTCATAGAA CAGTTATTAA ACAATANAAA 200

ATGTGTT 207

5 (2) INFORMATION FOR SEQ ID :401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :401:

GAGGCATGGC CACATTCCAA GAAATGGAAT AAGGAGTGGG ACAGCAGGCA 50

GGGGGCCAGC CTGGGGCCTG GGCCTTTTAA TCTAAGGACT GGGGAGAACC 100

20 AAGGGACCTT AGAGGTCCTC CAGTCCTCCC CATATNNAAA GAGGGAGAAC 150

AAGCCTGGAG AGGAGGCTAC CTTAAGACCC TAAGAAGAAT TTAGCAATCG 200

25 NTTCTCCAAA GATAGCC 217

(2) INFORMATION FOR SEQ ID :402:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 225 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :402:

TTTACAATAG ATTTACCTT CANTTTAGTC AGAGTTGTTG ATTCAAGACT 50

40 CTTCCACAC TCGCACATCG AAACATTTTT GTGCCAGGGC TTTCCAGCTC 100

214

CAATTATCTT CTCGACAGCA TATACAGAAT CCCACATCT GGAACACTTC 150
TCAGCACCTC CATANNTTGA GCAAATTTAG AAGTGTGGG ATTTGTTGTA 200
5 GGCCTGTGAG GCTGAACACT CTCTG 225

(2) INFORMATION FOR SEQ ID :403:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :403:

AGAAGGGGCA TACTCGCTGG AGACCTGGTG CCTCTATCCA CTGNACGCTG 50
20 ACTGNGGCTT CCACTGCGCC CGTGACNTT ATCGAAGCTA CAGAT 95

(2) INFORMATION FOR SEQ ID :404:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :404:

35 AGGAAAAATT GACATTACTT GTTAGAAGAG CAACTCTGAA AGAAAACAAG 50
CAAATTCCAA AACAGAAAAG ATTCACAATN NAAAGGTGCA TACATTAAAG 100
GGCCACACTG TGTAATACTG TGCCAACTTA TGCGAGTCTC ATTGTTTCAGG 150
40 ATGAAATGTG AGATTGTAGT TTGAATGCTA TAAGCAGGTT CCAAGATACC 200

215

CCAAATGACT GTAAGCCAGA CTNGAAGCAT GTCAAAAAG

239

(2) INFORMATION FOR SEQ ID :405:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :405:

15 GGCTATTATT CTAAGTGAAG TAACTCAGGA ATGGAAAACC AAACGTTGTA 50

TGTTCTCACT GATCATTGAG AGCTAAGCTA TGAGGACTCA AAGGCATAAG 100

AATGATACAA TAGACTTTGG GACTTGGGAG GAAGAGCGGG AGTGGGGCGA 150

20 GGGATAAAAAG ACTACAAATA TGTGCAGTGT TTA CTGCTC 189

(2) INFORMATION FOR SEQ ID :406:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :406:

35 CACCATCCTC CAAGTAAATC CCCCCTTAGG AAAGTAAGGG AAAAGACCCC 50

TTATAGCCCT GAGCTCCCCC TTGGA 75

(2) INFORMATION FOR SEQ ID :407:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 190 base pairs

216

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :407:

10 TATTCATCCA GCAGTGTTC TCAGCTCCTA CCTCTGTGCC AGGGCAGCAT 50
TTTCATATCT AAGATCAATT CCCTCTTTTA GCACAGCCTG GGGAGGGNGT 100
CATTGTTCTC CTCGTCCATC AGATCTCAGA GGCTCAGAGA CTGCAAGCTG 150
15 CTTGCCCAAG TCACACAGCT AGTGAAGCCA GAGCAGTTTC 190

(2) INFORMATION FOR SEQ ID :408:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :408:

30 GAAGACATGG CGCCCTAACA CTCGAGACC TGCTGNTAAA TAAAAGCTA 50
TTTTTCATTA AACCACCATT TCCTCCACCT ATTGGAGTCA AATATGAAAG 100
CTGTCGATGA AGCCTGNCTG GCTGCACAAG TTNGACTGNG TCTGAATAAG 150
35 CACTTTCATC ATGGACTAAG AATCCTTGGT GTGGNCNTGA TCTT 194

(2) INFORMATION FOR SEQ ID :409:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

217

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :409:

GCAGCACAAG AGTCATCCAT GGATACAGTT CCAATCATT TAACCACTTC 50

TAAAACAAGA TCATCTTCTG CAGCACCTGG TTTAGTTTA TCCTTGA 97

10

(2) INFORMATION FOR SEQ ID :410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :410:

TTTGAGCTCC TGGACCCTTC TTTGCCTACA CTGGCCTTCC TCTCGGAGGG 50

25

ACAAGGAAGC TGGCCTCCCT TTACTCTACC NTTNNTTNTG GTCCAGGGCC 100

AGCTCTTCCG AGGCTCCAGC CTGCTTTTCG CCGGTGTCAT CAGATCATGC 150

TTTGC 155

30

(2) INFORMATION FOR SEQ ID :411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :411:

218

5 AACGAAGNGT TCCTGAATAC CACAGCCTGC TGGGAAATGA CTAGGCGGTA 50
AGGTTCTGCC ATGCCTGTGA CCCACCATGG ACATACTGGA CCTTAATTCC 100
5 TCTGCTTCTG TGCTCCCTCC TGAGAACCCT TTATGAGCCT GATTCCTCAG 150
TCTCACCAGA ATTCTGGATC ACCCAAGAGG AAAAGACTGC CAGTTCTAGA 200
TTCCTCTATA GGGAGACCTG GATTGTTGAC CAGGTGAGAA GCCAATGGT 249

10

(2) INFORMATION FOR SEQ ID :412:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :412:

AGAAGGAGAC AAAACACCTC CTCTGTAATA GTACCTCGAA TGGATTGAGC 50
25 TTTACTCCTC TATAACTCAT CTTACACCCN GCATATTTAA ACAAACTAAC 100
AAAATGAAAT ACTAATAGTA AAAAGGCTGA CCCATGTGGC TTT 143

30

(2) INFORMATION FOR SEQ ID :413:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :413:

GGGTCCCCC ATTACGTAC TCCATCACAA AGTACAGGCG GTCCATGGTC 50

219

5 TGGAAGCAGG AGTGGAGCTG TCAGGAAGGG CGGCTTCCCG GGCAGGCCAA 100
 CACCCACTTC TCCACCATAG TGCCTCCAC GTCATCATCT GATCACAACG 150
 TCCTTCTTCA GGATCTTCAC AGCATAGAGC TCATCTGTGC CTTTCGTTCT 200
 GAAAGCATGA CCTTGCCAAA GCTGCCTTTC CCCAGCACCA TTAGGAAGTT 250
 AAAATC 256

10

(2) INFORMATION FOR SEQ ID :414:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :414:

 TCGCAAAAGA AGNGTACCAT AACTCCTATT TCNAATGGCT GATTGTAGTA 50
25 GCACTGGAAG TTTATCAAAA CCCAGGTGTA AATATGC 87

(2) INFORMATION FOR SEQ ID :415:

 (i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :415:

 AGAGGGGGAC CAATCTAACC ATCGCTCTTC CAGTCCTACC AGCACACTCT 50
40 TGCAGCGCCA TNCCACTCCC TGAGCTCAGG ATCCTAGCCC GCCCCCCCCG 100

220

GGATGCTAGT NNNCTCCACC CTNCCCACCT GTCATACCTG TGTANTACAC 150
ACCCACCCGT ATCACGCAGG ACATGAACCA GCACCACTAA GGCCCCGGNG 200
5 CAGTGTCTG NNNTTCTTCT CTANCTGTCT GCCCTGAGTC CCGGACC 247

(2) INFORMATION FOR SEQ ID :416:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :416:

TCTAGCACAC AGCTGCGCTC ACAAAAACCTG CGCGACTTGT TAGAACTAAT 50
20 TGAGTGGAGC CTGCAGGTGA GGGGAGGGAG GGGCTGCAGG TCAGGTAAGA 100
TCTGGAAGAC AACGCACACT TGAAGGGCAG GGGACTCTAA GCAGGGATTT 150
25 ACATTGAAAG GA 162

(2) INFORMATION FOR SEQ ID :417:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :417:

CAGAAGAAGG AGAACTCATG ATTCCAGAGA GCTTTGGGGC TTATTTTAA 50
40 GTACTTAGCA AAATATTTGT TTTNCGTGAT TTAGCTTGTC ATTAAACNAA 100

221

GAGCTACTG

109

(2) INFORMATION FOR SEQ ID :418:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :418:

15	GGATGTAAAT TATATGTTGT TTAAATTTT CCAGCATCTG AAAACCTTAT	50
	CTGCTAGACA ATGCAAGATT CACACAGAGT TATCTGGGAT TCTGATTTTT	100
	TAAATAGTAC ATATCATTAA ACCATT CNTT CTAAANGTAA GAAGAGCAGA	150
20	AAAAATCTTA TAAGATTATC AGATTTTCCT AATGACACAG AAATGNAAGA	200
	AA	202

25 (2) INFORMATION FOR SEQ ID :419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :419:

	TAGCAAATGT GGATTACAAG CAAATACAAC AAGTCGTGCC CCTCCAACCC	50
	ACCACAAACT TCTAAACGCC ACTCAGCAGA TGCATAGGAT TCGTTACACG	100
40	CAACGATTGA AATAAAAATA AAAGCTNCAA ATGCAATACC CANACTAGCC	150

222

TA

152

(2) INFORMATION FOR SEQ ID :420:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :420:

15 CAGCCCTACA CTCGCCCCGCG CCATGGCCTC TGTCTCCGAG CTCGCCTGCA 50
TCTACTCGGC CCTCATTCTG CACACGATGA GGTGACAGTC ACGAAGGATA 100
AGATCAATGC CCTCATTAAA GCAGCCGGTG TAAATGTTGA GCCTTTTTTG 150
20 CCTGGCTTGT TTGCAAAGGC CCTGGCCAAC GTCAACATTG GGAGCCTCAT 200
CTGCAATGTA GGGGCCCGG 218

25 (2) INFORMATION FOR SEQ ID :421:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :421:

GATGCCAATG TTTCATCCAC CGGCTGCACA GGCACAACT CCCCCACCCA 50
GGACGACTGT GATGAGGTGG CCCTCCCTGT CAACCCTGGT CCCTGGAGTC 100
40 CCCAGCACCT GGGGCCCTGA CGGTCTCGAT GTCACAGGCG CTTACTGTGC 150

223

TGCTGGCTGT CCTATGCCAG CCTCACCCAT GTGGGGACCA CGNAAGGCAC 200
ACTCCCTCAC CCCGGTGCCG GGCCGTGCGA TCCCCCA 237

5 (2) INFORMATION FOR SEQ ID :422:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :422:

AGNGTAATA AATACTGCAT CCTTCCACA ACATAGCAGG AATCTTATAG 50
GGAAATCCAT ATAGTTTCTG AACATGTATT NATATACTAA GTCTATATTG 100
20 TTTCTTTACG AAGTGTAAT AAGTGCTGCA CCATACTGTA AACAAACTC 150
GAATATTGAC TAAATAAAAT CAAAAGTTCA TCTGTAGTC ATGTCTTTCT 200
25 CC 202

(2) INFORMATION FOR SEQ ID :423:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :423:

GGGACACCAT TACCATCCAT TGACATCGCA TTTCCATAGA AATGCCAAAG 50
40 AAAGAAGTCC TGGGGTTTTT CATAGAAAGC TCAAAAAGTT CAACCTTTGA 100

224

.. TGCTATCCCC CAGCCCAATA CAAAATACAC AAAAAAGCAA TTATCAAAAT 150
ACTGACTTCG GTTCTTTTT CTCTTCAAAT NCCTATAATN GCTTTACATA 200
5 TTCGTATCAG CACCTA 216

(2) INFORMATION FOR SEQ ID :424:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :424:

CGACGAAGGG AGTACTCGCG CTTTGTCTCC CTATCCACAC TTGAGCAAAT 50
20 GCTCGCTGGT CTACTGCCAA AACCCATTTC ACCAACCATA TGTCCCTCGC 100
CCATACCCCC TCTCCCTCTC AAACCCTGGG GACAAATTCA AGGACCCAGG 150
25 GGTGCCCTTT TAAAAAAA 168

(2) INFORMATION FOR SEQ ID :425:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 35

(xi) SEQUENCE DESCRIPTION: SEQ ID :425:

TCGCAGGAGA AGGAGTCGCT TACTATGCAT CCAAAGGCTA CCGTGGTTAC 50
40 TCCTATATGA CATTCCAGAT TTTGATGACT AGCACCCACC CCACAGCTGA 100

225

GAGGAGTCAC AGTGGAACCT CCCAGCTTTA AGATATCTAG CAGAACTAT 150
AGCTGAGGAC TAAGGAATTC TGCAGCTTGC AGATGTTTAA GAAAATAATG 200
5 GCCAGATTTT TTGGTCCTTC CCAAAGATGT TAAGTGAACC TACAGTTAGC 250
TAATTAGG 258

(2) INFORMATION FOR SEQ ID :426:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :426:

20

TCCACATCAT CTCCAAAGCC CATAGGCCGA GAAATGGCAT CTGAGATCTG 50
CTGGGCCACC TCCTGTTGTT CCGTATGTCA GTCATCAGTT CATCTACCTN 100
25 GTCAATGTCC ATGTCCTGGT AGGCCTTCTT CATGCTTTGN CAGCAAGCTC 150
CATGCACGAA GGA CT TCTGC ATTGGTAGTG GCATTCTCAA TAGCCTCAGC 200
CTGAAACTCC AGGGTGGATA ATGCCCCGTC AATTTGTGCC AGCTGCTGTT 250
30 CGAATNNTTT TCTTTCTCGT AAAGC 275

(2) INFORMATION FOR SEQ ID :427:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

226

(xi) SEQUENCE DESCRIPTION: SEQ ID :427:

CTCTGTGCCT CGCTGAGGAA AAATAACTAA AATGGCAAAG AAGATCCTAA 50
5 GAAGCCGAGA GGCAAATGT CATCATATGC ATTTTNTGGC AAAGTGTGG 100
GAGGAGCATA AGAAGAAGCA CCAGATGCTT AAGTCAACTN TAAGAGTTTT 150
CTAAGAGTGC TC 162

10

(2) INFORMATION FOR SEQ ID :428:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 220 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :428:

ATGCAGAAAA GGAGTCGTGA GCGTAACACC CTCGCTGCTG GTCATAAAAC 50
25 CCATAGTTCC TGAATCATC AAAGAACTTA ACTTCCTGAC GCCAGATATC 100
TGCCATGCGC GAAGGGNTGA TACCACTCAG GATTATGAAT TTTGTTTAAA 150
GTCGNGTTTA CAATGATTG NCCTGGACTG AAATTCANGC TGCCTTAAGG 200
30 TGCTGATGAT ATTGAGAAGT 220

30

(2) INFORMATION FOR SEQ ID :429:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

227

(xi) SEQUENCE DESCRIPTION: SEQ ID :429:

5 GACTCATCTT GCCCAAGAAG AGCCAGGATA TGAGAAGATG GGAGAGGGAA 50
GGGGAGGTGT GAAACGTGCT GGTGCTTCCT GTCCTCATGG TGTGATGGCT 100
GCCCAGGCTG CTCCTTCGAG GCAGGACAGG ATTCCCATGG GAGATATGAG 150
GACCATGGTG ATTTCCAGGA CCAGTTATGT CCAGA 185

10

(2) INFORMATION FOR SEQ ID :430:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :430:

GGGATGCCCT GACCTGATGG CCCTTGACCA ACATGGTGCT GGAGGAGCAC 50
25 TACCTGGTCG TGGGAGTAGT GGTTCATCGTG GACCCAGGGG TGATCCCTAT 100
CAACTCTTGG GGTGAGAAGC AGCGCATGCA CCTGCGGGAC GCTTCCTGGC 150
TGACCAGCTG GACCCCATCT AGTCGCCTAC AACAGCGAGC CAGCACACCG 200
30 GCCCAGGTGC CGGAGATGAA TGAGCCCCAG CAGTCCAAGG TGTGATGTGG 250
GAAGACACCG CAGAGCTCAC TTACCAA 277

35

(2) INFORMATION FOR SEQ ID :431:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

228

(xi) SEQUENCE DESCRIPTION: SEQ ID :431:

5 AAAGTGCCT TGGGCATCCT GCCAGCCTGC CATGTCTTCA TGCCTGGTC 50
GAAGGCAGCC NGGACTATGG CCAGGAGGCG AATGTAGTCA CTCAGGAGCT 100
CAGCAAGGAG GAAGAAGTCA TTGTT 125

10 (2) INFORMATION FOR SEQ ID :432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :432:

GCCTAACTGT CAAAGCACAG AAAAGTTAAC AAAGGGTGGG ACTCGCCATT 50
TCGAAATAGC ACATTTTGTAG CAATAGGCTC TCTACACTAG AGAGCCAGTA 100
25 GACTGATATT CTTTAATGCC AGTTTCCTAG TTAATCGTAA AGATAGACAC 150
AATTCCCCC TTTATAAAG CTTCTGTCGT TTCACATAAT GACTTTAACT 200
30 ANAANGGAAA TGGGGCAGGA CA 222

(2) INFORMATION FOR SEQ ID :433:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :433:

229

CCATGNCGGC CCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT 50
 CGATTTCTTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC 100
 5 CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT 150
 TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAACTGT TGGTNTAACT 200
 NGNCGTTTCC TCT 213

10

(2) INFORMATION FOR SEQ ID :434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :434:

CCATGNCGGC CCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT 50
 25 CGATTTCTTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC 100
 CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT 150
 TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAACTGT TGGTNTAACT 200
 30 NGNCGTTTCC TCTGCCGGTG T 221

(2) INFORMATION FOR SEQ ID :435:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

230

(xi) SEQUENCE DESCRIPTION: SEQ ID :435:

ACACTTGATA CTATGCATCA AAGGACGTGG AGAACTAGAG CGGGCTACAT 50
5 TAGTATATTT TCGTTGTCAG 70

(2) INFORMATION FOR SEQ ID :436:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :436:

AGTACGCAAT GCTTTCTTAC AGTAAGCAAG AGCTCCTCTG TAATCCTTCT 50
20 CGTTGAAGGA AATGCAAGCT TTACCAAGAA GGGCTGGAAT ATTATTCGGA 100
GACTGATTGA GTACAAAATG AAACTGTGCG TCAGCTTGAT CCATTTTGTC 150
25 ACCCTCAAGT AGG 163

(2) INFORMATION FOR SEQ ID :437:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :437:.

TGTGGCTGAT CATAAGAAAG GAGCAAAGAA AGCTAGAATT GAAGAAGATA 50
40 AGAAGAAACA GAGGACAAAA AAACAGACGT TAAGGAAGAA GATAAATCCA 100

231

AGGACAACAG TGGCGAAAAA ACAGATACCA AAGGAACCAA ATCAGAACAG 150

CTCAGCAACC CCTGAATTG 170

5 (2) INFORMATION FOR SEQ ID :438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :438:

AGAACTACAG AAACCTGGCC TCCCTGAGTT TATCCTATGG GGGGCACAGG 50

AAAGAGCCCT GGACCATAGA AACCAAGTAC GAGTAGCAAG AAAACCAAAA 100

20 GGGTGGGAAT GGATCAAAGG TGTGAAAACA GATCTGTCTC GTAAGTGTGT 150

AATCAAGGAA CTAGCACCAC AACAGGAAGA TAACCCA 187

25 (2) INFORMATION FOR SEQ ID :439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :439:

AAAAGCAACC AGGTCGAGA AACAATAGTG TATGTGTTCC TATAGGTATG 50

AGTTATTCAN TGTAATTCG TTTTCTGCA ATCCTCTGCC GAAATGATNT 100

40 ACACTTACAA TGNNGAATGC CATAGGACAC TACAATCTGA ATCAAAACAG 150

232

TCGCGTCTGA AATGNTNGTG TGGTAGACCA CCCCCATTCA AGCCTTCATA 200

CTTCGTAAAA ATGCAAATGT TGAAGATCGN NTCT 234

5 (2) INFORMATION FOR SEQ ID :440:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :440:

GGACCAGGAA CCTAACTGAG ATAAGTTCAG CTTCCAGTT GACACCAAGT 50

CATCTAGTCT TCCCGGAGTA GATATAGTTG AGGTACTCCA TTCCCCAAA 100

20 CAGAGAGCTG ATCCCGGGCT GCAACACCTC CAATAGTCGA AGCTCCCTTA 150

ATNAAGGATA TCAATGTATT TCTTAAACGC TTGATGTCGT TCAAAGTCTG 200

25 TTC 203

(2) INFORMATION FOR SEQ ID :441:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :441:

GTGATGCACC TGACATCCCC TCACAGGCTC TTGGAGAACT GTAGTGCAAC 50

40

TCACTTAACC GCAATGCTGA GAGCAGAATT CTGGAGTATG ATCCAGGGGA 100

233

ACGTTTCCCC ACACCACCCG AGCTACTTTA CCAGCGATCA TGATTGTGAT 150
GGAATAGGCT TATTAAGTTA CACATTAAAA AAGTCATTAG AACATCTCGT 200
5 TCTTGACAC TAGTGTAGAA AGGTCTTCCA AAGATAAAAG GTGTAGGCCT 250
GGTT 254

(2) INFORMATION FOR SEQ ID :442:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :442:

20

GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG 50
CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG 100
25 CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGC 147

(2) INFORMATION FOR SEQ ID :443:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :443:

GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG 50
40 CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG 100

234

CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGCTNC 150

TCCGNGNGAG ACGCAGTGA CTNCGATGNT TAGCNCTAGT NNCCCGCT 198

5 (2) INFORMATION FOR SEQ ID :444:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :444:

ATACTACGCT AGGAGAACAA TGTCCTACA TATTATGGGT AGTGAGACAT 50

TATCTGTATA CAGGGACTGT GATTATTTAA AATATGCAGA ACTTATTTC 100

20 TCTGTGCTTT AGAAATAACT GTATACAGTG TTATAAGTGA AAGAACTCAA 150

AATAACTAAT ACCAAATATA CACCTATGTA TTAGAATTCA AAAAGCTGCT 200

25 TTCTGTGA 208

(2) INFORMATION FOR SEQ ID :445:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :445:

AGCACATTC ACTACGGGNT ATGTGCATTC TGGGCTTAGT AATGTCAAAT 50

40 CACTCTTCTC TCCAGCTTGG CCATTCCTCA TTCCTTGCGG GCCTGCCCTG 100

235

.. TAGACCACAG GCTAATGGAA TGTCCCGGTC TGNGTCATCA NATTCTGTAA 150
CCTGNAGCCC CCGCTGAG 168

5 (2) INFORMATION FOR SEQ ID :446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :446:

AGGCAGAAGG GACGCTACTG ACTTAAGCCA AACCCCTGATT GGTGGATAAA 50
GTATTCAGTT GTTCCATTCA TGCCTATCCT TTNTACAGCT CTCGCGACTA 100
20 TAACAAACAA CTGATAAAAT AGCATCAGTC CCTCCACCAG GTTGCCCTCA 150
AGGAAGCCAT GTTTGTGACG ATCCGACCAG TCCCTGACGA TCTCTCTAGA 200
25 CCACCCTGAC CTCGCCGAGA GTGCTGAAGG AGCTATCTAA CCA 243

(2) INFORMATION FOR SEQ ID :447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :447:

CAGTCAGGGT CACAGAACAG TATTCAAAAT GATTGCCAC CTGTTTTAGA 50
40 AATCTAAAT NNTAAGTAAC TAAGAGCAAA GTGCTATGTG GGTTTTAGAC 100

236

CATGACTGTT TGTTTGCTCT CCTGCCCTAC CACCAAGCAA AGCAGCAGGG 150
CTCCTGGGGG AGAGGGATTT CAACCCCCCT GATGGCAGGG GTGCTCTGG 200
5 GGAGGAGAGA GGAGAGAACA GGCTGTTTTG GAAAATATCC AGCACTTTGA 250
C 251

(2) INFORMATION FOR SEQ ID :448:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :448:

20

ACACTCCAGA NCATCCCACT AGAAAAACAA TTNGCAGGA ACGTGATGGC 50
AACAATCAGC AGCCAATATT CTCAAGAGTT CCTAATCACC AAAAACATAT 100
25 ACAATNTAGT CTAGAAAAAT AAGTCAATTT CATAAAATAA GTTTTTAGAT 150
CGAAAAGCAC CCCCTTCACA GGTACAGAGA TACTGAAAAA TAGTCCCTAA 200
AAATCTACTC ATAGTTTACG GAGAGAAAGG CATGCCATGT GAGTTACGGA 250
30 GTG 253

(2) INFORMATION FOR SEQ ID :449:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

237

(xi) SEQUENCE DESCRIPTION: SEQ ID :449:

ATATAAAAAA GATCCGCATA ATAAACCAAA TCAGAAAATA ATACCTTGTA 50
ATACCTCTGT AAGAAGCAGA ATACACCATA TGTTATTCAC ATGTATAGGA 100
GTGATAAGAA AAT 113

(2) INFORMATION FOR SEQ ID :450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :450:

TAGCATCCAG GGGAAGTTAA TCAATACGCG AAAAATACTG AAATTAAAGA 50
GACAAGTAGA AGAAAATGAA ATAATCAAGA GATTGAGAAA AGTTGCCAGA 100
AAGCTTGGAG AAAAACCAAG ATATGTAATT TTCGCAGAAG TCAAAGGTAG 150
AAACTATTTG AGATCAAAGT CCTATAAACA AAGTTAAATG ATTCCAAGAG 200
GTAAATAGGA G 211

(2) INFORMATION FOR SEQ ID :451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :451:

238

CTCCATTAGC TTTATGGGAC ATACGACGCA TAAAGATACT NTCCCGTGCG 50
NATTTACAC NTGNCAGAGC TATAAACCGG TGNATGATGT GATTTNCTG 100
5 TAGAATGATA TGGCCTGATA TGGAGGCCTC TTAATNGGCT TTTCAAGCA 150
GCAAAATGGT CTTGNGTGAG TCGTGCCGAG GCTNNNGATC AAAG 194

(2) INFORMATION FOR SEQ ID :452:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :452:

20

ACTTCAAGCT CAACCTATTC TCGTTCTCTT TGTTAGAGGT GTATTGAGGA 50
TAGCATATTG AGAATATATT CTCTGGTTCA AACCAAAGAT TTTGTGACAT 100
25 TAAAACTACT TGAATTTCTA CTTCATAATA GGAGTCAGTC ACTTCTGGGA 150
CTATAGTGAT GCTTGCAA 168

(2) INFORMATION FOR SEQ ID :453:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :453:

40

CGATTCTTGC CCTAGTCAGA GACTATAGCA GCCCCCAGAC GTGAACCAAT 50

239

TGGCCATCTC CAGAAAGTTT AACAAAACCC GACCAGGTTG CCCCCTTCAC 100
TTTCTTACAA CCTCTTCCCC TTCCCCAGGG GCTCTGCTCC TCACTCCAGA 150
5 TCATCCTTTA GTTTAGAGCT GCGCAGTGAA GTGGATATCA CTGAAGGAGA 200
TAGGACGCCA GACTACACTG 220

(2) INFORMATION FOR SEQ ID :454:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :454:

20

GCCATCCTTG ATGGAAAAGA AACTGAAGAG AAAAGACAGC CTGTGGAAGA 50
AGCTCAAAGG TTCTTTGAAG AAGAAGAGAG AAAATATGAC ATGATATCTT 100
25 TGCTTTTGAG TTCCTCACGC TCTCTGAATN TTATTGGTTG GACATTCCAT 150
ATGTAGCATT CTGCTTCAAT ATTATCTATT ATGTGTCTCT CTCTCTTCAA 200
ATANNTGCCT GTAGGTAAAA GCAAGCTCTG CATATCTGTA CCTCTNGAGA 250
30 TAGTTTTGCT TTGTCTTTAG CGGTT 275

(2) INFORMATION FOR SEQ ID :455:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

240

(xi) SEQUENCE DESCRIPTION: SEQ ID :455:

	TCGCAGAAGG AGGAACGGGG ACTTTCCATC CCCTGAACCA AGGCATGTTA	50
5	ACACTTGGCT CCAGCATGTT GTCATCATTC AACCAGAAAT CGCACAAATG	100
	CTACTGTGCC GGGGTGNAGC CAATTTTCTT AAGTAAGTGC TGACTTCCTT	150
10	AACANNTATC TNTNTTNTGG CTGTAGGGTG GCTCAGTGGA ATCCATTTTG	200
	TTAACACCGA CAATTAGTTG TTTCACACCC AGTGGTAAGC CAGAAGGGCA	250
	TGCTCTNGGG TCTGCCCATT	270

(2) INFORMATION FOR SEQ ID :456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :456:

	TCGCAGGAGA AGGAACCTTG ATGATACCAT TATCCTCACT TAGATGATGC	50
30	ACGACCCCTG CGCTGGATAC GGCGACGGTT TCTCATTTG CTTTGCCAG	100
	CTCTCATTCG CTGAGGGGCA TAGACCTTTT GATATCATCC AGGCTTTAGT	150
	TTCTTAAGGA GCAAACAGC TTCCTTGNNC TTCTGTAGC CTTCAACTTA	200
35	TTTAACTAC CAAGGAAGTT CAGGAAGTTC CTCAANACGA TGACCTTTAG	250
	ACAT	254

(2) INFORMATION FOR SEQ ID :457:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs

241

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :457:

ACACTA	ACTG	TTCCAT	CCGT	TATATTT	GCT	GTGAGG	AAAA	TTAAGAT	TCC	50	
10	TGTTGT	ATGG	GCTGCA	CTGT	TTCTGGA	AGA	CTACAG	AAAA	TCTAAC	ATGG	100
TTGACA	CTTC	CTGGTA	GCCC	TTCTGT	TACAT	ACACAC	CACAC	AACCA	AAGAG	A	150
15	GAAGAC	AGAG	AGAAA	ATCCT	GGTCCA	AAAG	ATCAC	ATGAC	CTTACT	AGTG	200
TTTCCC	CAAT	GACTGT	AATT	TATAAA	CTAA	AAATTG					236

20

(2) INFORMATION FOR SEQ ID :458:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :458:

GAGANN	NNNT	NNGGNA	AATG	NTTNC	GCACT	GNAGCT	AAGA	ANAGNN	ATGG	50
NNNTAG	GGNG	NNAGAN	GNCN	TGAAC	AGAGA	AAGCNT	GAGG	GCTCT	GGGAC	100
35	GCTGGT	AT								108

(2) INFORMATION FOR SEQ ID :459:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

242

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :459:

ACCCATGGCA AATAGGAAGA AGCTCAGTAT CGGCTCCTCC CACCATAACC 50
CCCACTTCTC CCGCCTCCTG GACCATAGTT TCCTCCACCA TACGGTCCCC 100
10 CCATGTTCTT GCTACCACCA AAGTTTCCAC TCTCCATTGG ACCGTAGTTA 150
GAGGT 155

15 (2) INFORMATION FOR SEQ ID :460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :460:

TGCTATTTCC CTTTCATAAA GGCACACATT TGATCTTATC TTCTCTTACC 50
CAACACGCAG TGGCAGTGTG TATTTTCCTT CTCTTTTTTT GTTAAATATT 100
30 CTGGTTTGTG GAGGTTTACA GACATGTGTT AGTATATCCT TGCCTGCATG 150
TAGTTGTTCA TTACTAGAC 169

35 (2) INFORMATION FOR SEQ ID :461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

243

(xi) SEQUENCE DESCRIPTION: SEQ ID :461:

5 ACCNTGTTTA ATTANTGCGC GGGCTCGCCG TTTGCATACA ATGGCTTACT 50
 CAGTGCTNNC AGGCTGTGAG TNAATAGAGN GTGTATGACT TAATAAGCAT 100
 TTTATCAGCG TACCTTTTTTC GCCATGCGCT ACCTGCTATT GATGAAGGCG 150
 10 GCTTAGGGCA TCGAAAAACC TAAAAGTCGA GCTT 184

(2) INFORMATION FOR SEQ ID :462:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :462:

25 AGGAACCNTG TTTAATTANT GCGCGGGCTC GCCGTTTGCA TACAATGGCT 50
 TACTCAGTGC TNNCAGGCTG TGAGTNAATA GAGNGTGTAT GACTTAATAA 100
 GCATTTTATC AGCGTACCTT TTTCGCCATG CGCTACCTGC TATTGATGAA 150
 30 GGC GGCTTAG GGCATCGAAA AACCTAAAAG TCGAGCTTNG NNGTGCCGGN 200
 AACGGCTCTA NANTACTTCT CATTGTAACT AGAGTACCAT ATTCGGCCGT 250
 NNACTGNGTT GTTGGCGACA GATGT 275

35

(2) INFORMATION FOR SEQ ID :463:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

244

(xi) SEQUENCE DESCRIPTION: SEQ ID :463:

5 AATTCACTAT GCGTGGCCGC CACAGCTATN CTTGTCCTCC TGGATCCTGA 50
ACCTTGNAAG CTGCACTAAT GAGTTCAACG GGAGTGCTCT GGGCCCAGGT 100
GTCAGCTGTA GCAATGCCCC NGCTGCAACT GAAGGNGCCA GCAATGCTA 149

10

(2) INFORMATION FOR SEQ ID :464:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :464:

ATCATCAGCA GTGTTGCTCA GCTCCTACCT CTGTGCCAGG GCAGCATTTT 50
25 CATATCCAAG ATCAATTCCC TCTCTCAGCA CAGCCTGGGA GGGGGTCATT 100
GTTCTCCTCG TCCATCAGAT CTCAGAGGCT CAGAGACTGC AAGCTGCTTG 150
CCCAAGTCAC ACAGCTAGTG AAGACCAGA 179

30

(2) INFORMATION FOR SEQ ID :465:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :465:

245

CTACCTCTGT GCCAGGGCAG CATTTTCATA TCCAAGATCA ATTCCCTCTC 50
TCAGCACAGC CTGGGAGGGG GTCATTGTTC TCCTCGTCCA TCAGATCTCA 100
5 GAGGCTCAGA GACTGCAAGC TGCTTGCCCA AGTCACACAG CTAGTGAAGA 150
CCAGAG 156

(2) INFORMATION FOR SEQ ID :466:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :466:

20

ACATCCCTGG AAGGAGGGCC TGAGGGCCAG GGAGGGAACA AGGCAGGAGA 50
CTGCTGGTTC TGGTTTTGGC CACCTCACCC TTGGCCACGT CCCCTCCGGC 100
25 TAAGCCACAG CACAAAGCAG AGCCAGGCTC TGGAGGCCCA GGGCCTCACC 150
ACTCCCCTNT GTCCCCCAG CAGGGGGACA AAACAG 186

(2) INFORMATION FOR SEQ ID :467:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :467:

40

TNNNGATGAN TATANAAGCA TCATNGACGG TATTTCCCNG TCTTGNANTT 50

246

TNATCGAGAN TTTANTCTAG TAANTATATT AATNTNT

87

(2) INFORMATION FOR SEQ ID :468:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :468:

15

ACTAGAAGTA CAGCATCCTG CTGCAAAAAT GATTGTAATG GCTTCTCATA

50

TGCAAGAGCA AGAAGCCGAG ATGACACAAA CTTTGCCTGG TATTTGTTGG

100

AGCTCTCCTG GAATCACTGA AGAACTTCTG AGGATCGGCC TGTCAGTTTT

150

20

AGAGGTCATA GAAGGTCATG AAATAGCCTG CAGAAAA

187

(2) INFORMATION FOR SEQ ID :469:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :469:

35

AGGGCACCAT TACCATCCAT CTGACATCGC ATTTCCATAG AAATGCCAAA

50

GAAAGAAGGT CCTGGGGTTT TTCATAGAAA GCTCAAAAAG TTCAACCTTT

100

GATGCTATCC CCCAGCCCAA TACAAAATAC ACAGAAAAAG CAATTATTAA

150

40

ACATCGGCTT CGTTTCTTTT TCNCCTTTGA ATNTTAATGT TTACATACTA

200

247

GTGTGCAGCA CCTACTTCTT NATCGCCGTG AACTGAAATC TAGATTTTAA 250
ACTGAA 256

5 (2) INFORMATION FOR SEQ ID :470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :470:

CTCAAAACGA CAATTCTGTG CCTGGGGGAT CTGACCTGGT GAGGTAGCCT 50

GAAGTCTGAA TGGAGCCCAT AGTCGAAAAC AACCTAAGAA TCTCTCAGAA 100

20 GAGGGTTTG 109

(2) INFORMATION FOR SEQ ID :471:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :471:

35 GCGGCAGTAT ACAGAAGCCA TATCAGTTGG GAAAACTTT ATCAATCATA 50

GAGCCTTTTG AAGAAAAATT TGCCAAGCGT GGTTTTTTGC TTGNAGACCT 100

40 ATATATATTA CCTACAGGCT GAGAAAGCTT TGNATTTCT 139

(2) INFORMATION FOR SEQ ID :472:

248

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :472:

10

TCGCAGGAGA AGGAATGTTC CCAATAGGAA CGCCTGTAGA CTGTTTCAGAA 50

GAAATGCCCA AATGAGCCAG ATGAGAAGGC TGAGGGCAGG GCTGCTTTTG 100

15

GCTCTGAGGA CTATAGATTT ATCCTCTAGG TGATGAGGGA CTATTAACGG 150

CTGGTGAGTC TGGAGAACTG AACAGTGGA GCTCTATTTT AGATTCACGT 200

GGCAGTAGAG GATAGAGGTG TTTGGAAGCG GTGGGCAGTT GCAAGCTATA 250

20

TGGGAGACAT TT 262

(2) INFORMATION FOR SEQ ID :473:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :473:

35

ACAGAAGGAC TTTGTCTCTT TAGCTTGTTT AGCTCAATGA ACATTATCTC 50

GGCAAATGAC TCTGCTTTCT CGAAGGTCCT TCTCCGCTCC AGGTTTACTT 100

GCATCTCTCA TACTTNNTAC AGCCAACATG AACACTCTAT GTATTTTCTA 150

40

AGCTTTCNTC TGTTCAGAA CTTTGAATTT AAAACGTCT 189

249

(2) INFORMATION FOR SEQ ID :474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :474:

TNCGTGCCTA GCAAACCTAA ACTCGAACGC ACGTAATAGT GCTCATAATT 50
CTNTNAAGGA CTTTAAACTT TACTCNGTAT GCTNTNTTGA TGACTCTAGC 100
AGCCTCGCTA ACCTAGTTTA CCCCACTGTC CCCACCGGCG AACTNTTTGT 150
GTTAGTACGC GNGTTA 166

20

(2) INFORMATION FOR SEQ ID :475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :475:

TTTTTTTTTA GTAACACTAA AGAGCTGTAA AGAACATTGA AGGTGGTCAT 50
TCCTTCAAAA CTGTGTTTTG ACCACACAAG GTGGGCATTA ACAAACAAAT 100
TCAACTTAA 109

40

(2) INFORMATION FOR SEQ ID :476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs

250

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :476:

10 TCTGGGCGGA AGGTGGTGCG GTGAAAGGTG CAGGGACAGA CTGGGTTAGA 50
GGCCACTCTT GGTCTTATCC TCCATGGCCA CAACAGAGGT GACAAATACA 100
CGGGTCACTC AGTTACGTTT AGCCACAGCC T 131

15 (2) INFORMATION FOR SEQ ID :477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :477:

ACATGGATAG GTGTATGCAT ACTACGGCTA AGGAGAAACA ATGTTCTTAC 50
ATATATGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT 100
30 TAAAAATATG CAGAACTTAT TTCATCTGTG CTTTAGAAAT AACTGTATAC 150
AGTGTTATAA GTTGAAAAGA ACTCAAATA ACTAATACAA ATATACACTA 200
35 CGTATTAGAA TTCAAAAAG CTGCTTTCTG TGAAGTCAAT CAGCTATATT 250
AAAAAAGACA CAAAT 265

40 (2) INFORMATION FOR SEQ ID :478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs

251

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :478:

10	AATCTACCAA CCTTAAAGCT CCCGNGATAA AGCTGTATTT CCAAAAGACC	50
	TGTNTTTTATT NGNNGGNGTT NGCTTTCTTT GTCATCTAGA GCCTTGTTGT	100
	ACATGCAATG GGTGGGAGAT AGTGGTACCT ACTGTTGNNT CTNTCTGTGT	150
15	NTTCATCATG GTGTTGTCTA GGTCTCCTGA GG	182

(2) INFORMATION FOR SEQ ID :479:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 169 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :479:

30	AAGCCGTCGG GAGCCGCCGC CGCCATCTGA GGGAGGTACC CTGGAACCA	50
	CCTTTCACGG TGGGGAAGTG CAGTCGCGGT GGGCAGCTCT GGGGCCACGA	100
	AACGGGAGCC TCTAAATCTT GGTCTGGGACT GCTCGCCTGG AGCCGCACTC	150
35	TTGAGTCCGA GGCCATCTT	169

(2) INFORMATION FOR SEQ ID :480:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|---------------------------|
| 40 | (A) LENGTH: 238 bas pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |

252

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :480:

	AGATAACGCT CCCATCCCAG GCTAGAGACT CCATCTCTAA TTTNCNCAGT	50
	CCGTCAATGA GAGGCAGGGA CTGAAATCCC AAGTTCTGTC TCACCGGATA	100
10	TTTTCCAGGA ATGCCTCTCT TCCAAACATC AGCGACATTT AACAGACCCT	150
	GAGCAGCAAA CTTCTGCCCC AGAGGAAAGC AGAAAACCAA TTTATGTAAA	200
15	ATTAGAAGCG ATTTGCTTGA TCCATCACTN GCTTCCAC	238

(2) INFORMATION FOR SEQ ID :481:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 201 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :481:

	TCGCAGGAGA AGAAATCAAC CCCTGCTTCT CAAATCCAGA CAGGCCACAC	50
30	TGGCTAGAAC TTCCACCCAG CAGTCCTGCT CCTGCCCCGAA GTCTGCAAGC	100
	AAGTGAACCA CATGTCGCTA TGAAAGCACA CAGACAACAG ATTAGGGCAG	150
35	ACCTGGCAAA GATATGCCTG TCTGCCATCT TGGCCCCTGT CTGAGGGAGG	200
	C	201

(2) INFORMATION FOR SEQ ID :482:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

253

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :482:

CGGCTCAGNC TGTGGCGCG AAGAGAGTCT AACCCAAAAT TGCAAAACTC	50
CCGTTGATTT CCAGGCCCTA CCACACGGCG ATGTCAACTT GTCCTCCAGA	100
CATGGACGAC TACCAAAGAT CCCAGCTACG AAGCATGGCC TTGCTTAGAA	150
ACNTTTTATAG AT	162

(2) INFORMATION FOR SEQ ID :483:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :483:

ATATGAAGGA GGAAATGCTC GTCACCTTCG TGAATACCAA GACCTGCTCA	50
ATGTTAAGAT GACCCTTGAC ATGAGATTGC CACCTACAGA AGCTGCTGGA	100
AGGCGAGGAG AGCAGGATTT CTCTGCCTCT TCAAACNT NCCTGAACCT	150
GAGGGAACT TTGGATTCTC CCTCTGGTCG ATACCCACTC AAAAAGGACA	200
CTTTTGATTA GGACGGTTGA AACTAGAGAT GAACGGTTAT CAACGAACT	250

(2) INFORMATION FOR SEQ ID :484:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 base pairs

254

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :484:

10 AACATTATCT TGACAACTG AAGAACACTT CAGTTAACAC TACCTCGAAG 50
AACCATCAAT GACTTGCTTT GAACAGACTA TAAAAGGCAT TCTCAAGGAG 100
ATTAGAATGT TAATGCCACT TTGATTAGAT CT 132

15

(2) INFORMATION FOR SEQ ID :485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :485:

TGTGCGTGGA GACGGTGGAG AGTGGAGCCA TGACCAAGGA CCTGGCGGGC 50
CGCATTCACG GCCTCAGCAA TGTGAAGCTG AACGAGCACT TCTTGAACCC 100
ACGGACTTCT CGACACCATC AAGAGCGAC 129

30

(2) INFORMATION FOR SEQ ID :486:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

255

(xi) SEQUENCE DESCRIPTION: SEQ ID :486:

TCGCAAGAGG AGACATTCTG ATCATCCTCA CTGGACGCCA CAGGGGCAAG 50
5 AGGGTGGTTT TCCTGAAGCA GCTGGCTAGT GGCTTATTAC TTGTGACTGG 100
ACCTCTGGTC TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT 150
CATTGCACTT CAACCATATC GA 172

10

(2) INFORMATION FOR SEQ ID :487:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :487:

ATGCTGCACA CTATGTCTCA CAACTAAAT GGATCCATTA AAAGTTATGA 50
25 TTAAAAAGGC GACCACCCCC AAAAGAAGTC ATAACACTCA AGGGTGTCAA 100
TATATACAAC TGTGTAAACA CAACCAATCT ACAACTATAT CAACACAACC 150
AGCACTCCTC TATGGGCACA GACACACACA CAAAATTGTC CTTGCTTTTC 200
30 TCAGATATAT 210

30

(2) INFORMATION FOR SEQ ID :488:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

256

(xi) SEQUENCE DESCRIPTION: SEQ ID :488:

ACATGGATAG GCGTATGCAT ACTACACTAA GGAGAAACAA TGGTCTACAC 50

5 ANACGTAGTG AGAACATTAT CTGTATACGG GAACTGTGAT 90

(2) INFORMATION FOR SEQ ID :489:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :489:

ACCATGAGAC CTACATCCGA ATCTGACCCA GGCAAACATA CCGGGAGCCA 50

20 TACCGCACTA NCGGCTCTTC TCAAATCTCC TGGCCACNCA CCGAGNGCC 99

(2) INFORMATION FOR SEQ ID :490:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 30

(xi) SEQUENCE DESCRIPTION: SEQ ID :490:

35 GGAAACCTGG AGGTGCGCAT CCTCGAGTGC GAAGAGAAGG TCTTCCCCAG 50

CCCCCTCTGG ACTCCATGCA CCAAGGTCAT GGCCAGGAGC TCTTGGCAGC 100

TCAGCCCTGC CGCCCCAGAG CATGTGGCGG CTGCTCTCTA CCAGCCGAGA 150

40 GCTTCGGAGA TGCAGCATCT GCGGCGAATG CCCCCA 186

257

(2) INFORMATION FOR SEQ ID :491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :491:

AGCCAACTAA GTTCTCTCTT CGTGAAACAC AGGTCCATGA GTCGACACAA 50
ACACTAATGC AAGAACCATC ACGGAAAACC ACCGCAGCAG CTGAAACTTT 100
TATAGCCCAT AAAAGGACCA AACAAGTAAG CTGAATGACT GTGAAAATAT 150
GACCTTCCAG AGCGGCACAT AACAGGATAT CAAATCAGGC TGATGCTTAG 200
CAGGCTTCAA ATATNATGGT CAAATGACTG GATTACTTAN ATGAGGCAAC 250
TTCATATCGG AAA 263

(2) INFORMATION FOR SEQ ID :492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :492:

AGAGTGGGGT TAGCTCTGCC TAGCGCTACA CAAGAAAACC TCCCTCCAGT 50
AAATNGGTGT GGGNGGTCCG CTTTGGCCA TCATCGCACC CCCCCGGTCA 100
CTGGGCGTTG TTGCCGGGCA CTTGTTTNNC NGGCTGGGTG TGTACCGTAA 150

258

CCGTGGGTC

159

(2) INFORMATION FOR SEQ ID :493:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :493:

15 GGGCAGAGNA AGAACTGTTC CACCAGGTGA ACAGTCCTAC CTGCTTGGTA 50
CCATAGTCCC TCAATAAGAT TCAGAGGAAG AAGCTTATGA AACTGAAAAT 100
CAAATCAAGG TATCGGGAAG AATAATTTCC CCTCGATTCC ACAGGAGGGA 150
20 AGACCACACA ATATGTNGTG CTGGGGCTCC CCAAGGCCCT GCCACCT 197

(2) INFORMATION FOR SEQ ID :494:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :494:

35 GATGGGGAAG GGCATCCCAA CACAGCCTGT GGATCCTGGG GCATCTGGAA 50
GGGCGCACCA TCAGCAGCCT CACCAGCTGT GAGCCTGCTA TCGGGCCTGC 100
CCCTCCAATA AAAGTGTGAG AACTCCACTG TGTGCCCTGT CTTTGGGCAG 150
40 GGAGGGCTGC TGTGAGTGGA GTCTTGAGTN GGTGAGTG 188

259

(2) INFORMATION FOR SEQ ID :495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :495:

ACATGACCAT CCGCATCCGC CTTTATTGAC AATGAGAAGA TGGAGTCCCCG 50
GACGCATCTA TCCCTCTTTG GCCCTTACAG GTTGCCACG AGAGTGAGAC 100
GCCTTCCTGG ACCAGGGGAG GGNGNGTTGG TNCTNTGNGC GTGNGGGTNT 150
GTGGGNGCTG CTGGGGAGG 169

(2) INFORMATION FOR SEQ ID :496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :496:

CAGAGAGAAC GTTCTATGG CTGCTGCTTC TAGGAGTCTC TCGCTCATAG 50
AAAAGGCACA CACTGAAAGA GGAAGCAGAT CCCATTGCTG TGGAAAGTCCC 100
ATTGTTAGGA AGCTCTGCTT TTCTGGAGTT CAAATTCGCA TTCATGATGC 150
TTTAAACCGT CAAGCTGGGT GG 172

(2) INFORMATION FOR SEQ ID :497:

260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :497:

GAGAGTGGGG TTAGCTCTGC CTAGCGCTAC ACAAGAAAAC CTCCCTCCAG 50
 TAAATNGGTG TGGGNGGTCC GCTTTTGGCC ATCATCGCAC CCCCCCGGTC 100
 ACTGGGCGTT GTTGCCGGGC ACTTGTTTNN CNGGCTGGGT GTGTACCGTA 150
 ACCGTGGGTC CTCTGACAAG TGCCTAACTC GGCCACCCC TTAGGGTGTG 200
 TNTCATCGAA GTGTAGNGAA TGGTGAACG TTTGTTTGTN GTGTGC 246

(2) INFORMATION FOR SEQ ID :498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :498:

CCCCCTTTAC CAGCAAGTCC TCTACTCAGA AAGAACTGAC CCACGCAAGT 50
 CTGGGAGAGT GACTAGTTCA AATGTGCAGG GCTGAAGCTT CCAAACACAG 100
 CCACTATTTT TGTTGTATAT CTCATCTCA ATGGCGACAT GGCCACTGCC 150
 CAAGGAACTT GTGGCAGGGA TCCCAAGGTG AGGCAGCAAC AGATGTCTGT 200
 GAACATCGTG CGTTA 215

261

(2) INFORMATION FOR SEQ ID :499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :499:

GATNGCCACA TCTCAACACT ATACNACTCG CTNTTCGAAT TCGCCGTNTT 50
AGAACCGCAA GAGACCTTGA TTTAGTCACG CGAGTTCGTC TTCCTGTTCC 100
ACANGAAAAT AAAGCTAGGG AGGTGATTTA TCTATCCGAG AAAAAAGCCG 150
GGGACTGGTG GAANNNGAAC AATGNTCTCT NTGTCGTACT ACAAT 195

20

(2) INFORMATION FOR SEQ ID :500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :500:

GCGGCCTTGG GGGCACCGGC GTGTCCTGCC CAGTGGGATT AAAAAATAAT 50
GCTCCCCACA TGGCGGGCCT TTGAGGTTCC AGTAAAAATG CTTTCAACAA 100
ATGGGCAATG CTTGTGTGAT TCACAATCGT GGCATTATAA GTGCACAAAG 150
TACAAAGGAA TTTATACAGA TTGGTTTACC GAAGTATAAT CTATAGGAGG 200
CGCGATGGCA AGTTGATAAA ATGTGACTTA TCTCCTAATA AGTATGGGGG 250

40

262

GTGGAGCTGT

260

(2) INFORMATION FOR SEQ ID :501:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :501:

15 AAAGGCATAG TAAAAATAAA ATCTACGTAA GTAACAATCT AATACTATAT 50
TAAATNCGTT GCTACAAAGT GTTTTGTTC TCTAAAAGT AGTTTTTGCA 100
TATCATTCGA CCTCTTCACC CATNTGCTGG CTTATTTGCT TTATATACAA 150
20 CAGTTAAAAT TTGTGCACTA AGCTGAGCTG CCTTCACAAT GTGGTTCAGA 200
CAAAATGCAC CCAAAGAACT ACATGTTAAG AGAGTTTATG TCCATGCTCA 250
25 ACCATGGCTT GCCCAAAT 268

(2) INFORMATION FOR SEQ ID :502:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :502:

AAAAACTCTA ATCCAGACTA CAGTTGTCGA GATTCAAGTC GTGAGTGCAG 50
40 GAGCGTACAC AGTGCCGTGC TGGCACATGC ACTGCACACG CTCTAGAGAC 100

263

GCTGACCTGG CTCTCGGAAA CGCAGGAGTC TTTCTGAGCC AGCTCAGAAA 150
CC 152

5 (2) INFORMATION FOR SEQ ID :503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :503:

CCCTGACCCC TCCTCACCAC CGCGCTGCAC CTCAGGGTTA CAAGAAGAAC 50
TAGGAAATAA CGCCGGCCAC CNGACCCCTG GAGAGGGGCC GGCTAGAACA 100
20 NTTCTAAGAT CCNGCACAGC AGGTCCCGNA TGTNGAACCT T 141

(2) INFORMATION FOR SEQ ID :504:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
30

(xi) SEQUENCE DESCRIPTION: SEQ ID :504:

35 CACACGACAC ACGACACGCA CGCAAACACG CCAGACGCGA CAGAGCGCGC 50
GCGGGAGCGG AGCAGCGGAA GCGCAGCAGC GCACACGAGA GATAAGGGCG 100
GCCGAGC 107

40

(2) INFORMATION FOR SEQ ID :505:

264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :505:

10

ACCCTCTTCT GATAAATTG AGGGCCCGTT TGTCCTTGA GACCTTCAGT 50

AACTCCATGG CGCGCCATCG TACGGGGCAA ANACACACCT CCCGAATCAT 100

15

GTCCCGCACG AACTTGGTGT GTTTGGTCAG ACGCCCGCGT TNGGCNTGTG 150

CTGGGCTTGC TCACGTTCTT GTCACTTTGT GGCCCTTGTT GAG 193

(2) INFORMATION FOR SEQ ID :506:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :506:

30

ACATGGATAG GCGTATGCAT ACTACGCTAA GGAGAAACAA TGTCCTTACA 50

TATTACGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT 100

35

TAAAAATAGC AGAACTTATT ANCTGTGCTT TAGAAATAAC TGTATACAGT 150

GTTATAAGTT GAAAAGAACT CAAAATAACT AATAAATATA ACCTATGTAT 200

TAGAATTAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA 250

40

TGACACAAAT CCAAACAAGA TGCA 274

265

(2) INFORMATION FOR SEQ ID :507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :507:

CAGGAGAAGG AAGGTTGTAC GTGGACACTA TAAAGGTCAG CAAATTGCAA 50
AGTAGTCCAG GTTACAGGA AGAAATATGT TATCTACATC GAACGGGGCA 100
GCGGGAAAAG GCTAATGGCA CAACTGTCCA CGTAGGCATT CACCCCAGCA 150
AGTGGTTATC ACTAGGCTAA AACTGACAAA GACCGCAAAA AAACCTTCAA 200
CNGAAAGCCA AATGTNCCAG CCGGAAAGGA AAGNGCATAC AAGGAAGAAA 250
CCATTGAGAA GATGCAGGAG TAAAGTATTA T 281

(2) INFORMATION FOR SEQ ID :508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :508:

AGGGNTGCTA ANNTATTGGT GGGCAGGAGG CATCGCTGAT GATCTTGAGG 50
CTGTTGTCAT ACTTCTCATG GTTCACACCC ATGACGAACA TGAGGCATCA 100
GCAGAGGGGA CAGAGATGAT GACCCTTTCG CTCCCCCTG CAAATGAGCC 150

266

CCAGCCTTCT CCATGGTGGT GAAGACGCCA

180

(2) INFORMATION FOR SEQ ID :509:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :509:

15

AAATGCAAAA CTCACCGTGC AACTCCTAG ATCCCTGCCA CAAAGAAATC

50

TTTGAAAAAT GAAGTCTTCC TTTCGGACAA TATACCATTN GAGTTTCTCT

100

ATTT

104

20

(2) INFORMATION FOR SEQ ID :510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :510:

GTNNATACAC AACTAAGTTC AAATAAAAAA ACCAAATNAA AAATNGGCAG

50

35

GGAAGCTAGA GCCAGAATCA GGAAATCTG TTCCTCGTC CCCAGACTCC

100

CGCCAAGCCT ACTCCACTAA CTAACANNGA CTCTATCAAG TTTCTATCAA

150

GACTTGCATC TGNATCTTGN A

171

40

(2) INFORMATION FOR SEQ ID :511:

267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :511:

10

ACTGTACCTA TCATCCTGAA AAACCTTATG GGGGAGAAAG GTCAGCAGCT 50

TCTCTTTCTT TTNATCGAAA ATAATAAAAC TGGGTATTCT ACTTTAACTA 100

15

AATGTAAGGA AGAAAATATA CAAGCCCATATA TTTAATGTAT TTCTATNCGA 150

GCAACAATAG TTCATATGTT CATGTTTGCT ACTATCACAA TTCAACATAT 200

20

GAACACAGAT CAGCTCTATA CCATGAATAC TGCTGGAAGT GATGGTTTAG 250

GATTA 255

(2) INFORMATION FOR SEQ ID :512:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :512:

35

GAAAGATTGG ACATGATTGC GTTTATAAGA ATGAGAGTGT TAAATTGGAT 50

TTCTTGCTTT ATTTGTGACA TTTCAGTTTA TTAGAAATCA TGTTACCATT 100

40

AGAAAAATTG AAGTTTCCTA GTAACAAAGT AATTTGATTT GTGTAACCTG 150

ATAAAAGATT TACTGACTTA AGCTTTTGTT TTTTTCATA AGCTGCTTTT 200

268

GAGCTTTGTC

210

(2) INFORMATION FOR SEQ ID :513:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :513:

15	CTGTACAATC ATCCTGCAGA AAATTGTTTT GGAGAATTCT TGGTAATTGA	50
	AGACCAGCAG AGCACCCCTC CCCACCCGCC CCGTAAAAGT GCTTACAATG	100
	AACAGGGATT CTTTTCTTTA CAAAAGACCC AAAGATACGT GGACAAAAAA	150
20	AGAAAAGCTT GAAGTCTCAA TGCCTAATGT GTGCACATAA AACAGGCACG	200
	AAGAAACAAA CGTGTGCATC CT	222

25 (2) INFORMATION FOR SEQ ID :514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :514:

	GCAGGAGAAG GAAAAGACAG CAACTCATCC CAGAATTGCC NAATGAAGAT	50
	GAGGAGAATC CCCTCAAAGG GATCTGTGTG CTTACAGTGG TGACAGTGAC	100
40	AATGAGGAGG ACTGATGAGA GACTCAAGAG TGAGGAAGAG AGCTAGCTGA	150

269

CTGNAAGAAA TGACCTGTCT NNTCTNCAGC GCCATTCCCN AACAGATGCC 200

CTAGTCAGGA CCACAACCTCT TAAACCTCAT AGCNAAATAT 240

5 (2) INFORMATION FOR SEQ ID :515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :515:

CAATGCCCAA TCTGAGTGTA TACACATCTT AGGAAAAATA ATCTAANGTA 50

ACTTTTGAGG GTGAGAGNGG AAATAAGAGA TCACATTTAT TCAAGACTGA 100

20 TCCCTATNAG GAAGGAGAGG CCCAGGCACA GATACCACAA AAGAGCACAG 150

TACCCAGCTG TCCTGGNATT GNTTGAGTGT AAG 183

25 (2) INFORMATION FOR SEQ ID :516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :516:

TCGCAGCAGA AGGAAGTCGT TGACCTGGCA GCCAAGGGAA CACACAAACA 50

CACTCACACA CACATGCACT CACCTGCATA CACACACACT CATAACACAG 100

40 AACACTCATA CACACANGCT TGTGCACACA TGTTCATGCA CATGCATGCA 150

270

CTCACACTCA TACAAACGCA CATTTAAACA CGTGTGNACA NTGTACTCAG 200
ACACACACAG GTGTG 215

5 (2) INFORMATION FOR SEQ ID :517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :517:

TCGCAGAGAA GGAACAATCA GGGCCATGAC AGGAACCGCA AAGAACCAGA 50
GGGTATAGGC AGCAAAGAAG GGCACATAAA AAGGCTGCTT CTCAGGAAAG 100
20 TGTCGCAGTG AGACAAACAC ACATACAGAC CACACACAGA CCACCACCTC 150
AATCATGGGC CCTAGCCGNC CTNGTAATAC G 181

25 (2) INFORMATION FOR SEQ ID :518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :518:

ATGTAECTCA ATCCATCCGC AAGAAAACCA AACCAACAGA AAAGGAAGCT 50
GAAGACATGG ACATCGCAAG CCACGCGGTA ATGCATACTT GGCACAGAGT 100
40 AGCCAATATA GAAGACGTGT GCCTCACACG GTTCACTTTG TTCATCAATA 150

271

AAAGAATATA AAAATCTCGT TCACCCAGTG GTAAGTGTAT TAAAATAGAT 200
CTGTATCATA CACACAGTTT CTCCCGGAGT CGTGAGAATG ACAGGAGGGA 250
5 CCTGGCAACT 260

(2) INFORMATION FOR SEQ ID :519:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :519:

AAGCTAATAC AATGGTCATT TCCAGACAAA TTAAAGGAA AACTAAGGC 50
20 TGCTTCAAAG ATTATCTGAT TCCTTTAAAA TATATGTCTA TATACACAGA 100
CATGCTCTTT TTTTA 115

25 (2) INFORMATION FOR SEQ ID :520:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :520:

CANGTGGCTT CAATTAAACA ATNAGGAGCC TCNNAACATC CTGTGCGAGA 50
AACTCCCAAT ATAAACGCCC CCANACACTA ACACAAAACA GCCTTATTAA 100
40 CCAGATAAGT TCTCCACTAC CACTCCTAGA TTTGATGTAA CCCTGAATNT 150

272

GACTNATAGN TNGACCCACC TGTGA

175

(2) INFORMATION FOR SEQ ID :521:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 136 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :521:

15 ATGGAATCAA ACAGCTCTAT AATGAAGATA ATGTCTCAGA AAATGTGGGT 50

TCTGTGTGTG GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG 100

TCCACCTTTG CAGCCTGTTT CTGTCATGTA GTTTCA 136

20

(2) INFORMATION FOR SEQ ID :522:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :522:

AATGGAGCAA TTCATCCAGT TCTTCTAGAA ACAGCTCAGA ATCAAAGCTG 50

35 GATATATTTT GTGTCTTCTG TGACTGTTCA TTCATGGAAG GAAGCAGACT 100

GCTTTGGGCA GAATTATTCT CCTGACTACT TGAGCTAGTA GACTAGGAAC 150

TATTCCATAA GAGGAAATCC TGTAAGTCTT AAATCCCCAC TGGAGAAAGC 200

40

(2) INFORMATION FOR SEQ ID :523:

273

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :523:

AGTAAGGTTT TGCATCCTTT GATCAGCAGG TAACTGACGA ATTCTTGAGT 50
CGAAGATTAT ACCTTGATGA GCTTTGATGA GCTCTTGCAA ACGAATGAGA 100
CCAGTGCTGT CATCATACAC AACCATGACG TTTTCCACTT GAAAAACTGC 150
ACCAGGTCTA AAATGCACGC TGAGTGAAGA GAAGTCTGGG CAGAGACTGA 200
CATA 204

(2) INFORMATION FOR SEQ ID :524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :524:

ATATCTGTCT CATCATCCCA AGGTTTCACA TCTAGTAAGA TGGAAGACTT 50
GGCAACAAGT GCAGGTTTTT TGGCTTTCTT TGATTCATAT TGTGCAAGAC 100
GTTCTTCCCT CAGCCTCTTT GCTTCTTCAC TTNNTCTAAN ATAATCCAAA 150
GAGGTCAATG TATCATCA 168

(2) INFORMATION FOR SEQ ID :525:

274

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :525:

AAACTGTTCT TTAAAAGGCC TCTCCTGGTT ATTAAGCCAG GAAGAGAAGT 50
 AGAATCTCGA ATCACCTAAN GGAAATGGTG ACACAGGTTG TCCTTTCTCA 100
 GCCGTTGGTT TCCTTTCATC TCTGAAGGCC TGTAGTACCA TGAGGAAAAC 150
 ATTTAATTTA GAGGGTGAAC CCAACAGTAG GAAGCTGAAA GCAGAAGTGT 200
 TTATCTCCCT CTGCATTCAG ACCAGGCTCC TTAGTGCACT CATCAGACTA 250
 TCGCTGCCCC TGCTGTCTGC TGTGAGCCT TCACCACCAC T 291

(2) INFORMATION FOR SEQ ID :526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :526:

CATCCGCGTG CTGGACCCCT TCACCATCAA GCCCCTGGAC AGAAAACTCA 50
 TTCTCGACAG CGCTCGTGCC ACCAAGGGCA GGATCCTCAC CGTGGAGGAC 100
 CATTATTATG AAGATGGCAT TGGTGAGGCT GTGTCCNNNN GTAGTGGGCG 150
 AGCCTGGCAT CACTGTCACC CACCTGGCAG TTAACCGGGT ACCAAGAAGT 200

275

GGGAAGC

207

(2) INFORMATION FOR SEQ ID :527:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :527:

15 AGCATTCCGT AAGGACGGAC GTGTTCAAGG ACAACTTTGA TGAGATGGAC 50
AGGTCTAGGG AGGTTGTTCA GGAGCTCATT GATGAGTACC ATGCGGCCAC 100
CCAGCCAGAC TACATTTCTT GGGGCACCCA GGAGCAGTGA TTTCCCTCCC 150
20 CACTACTTCT TTNCTTAGAT GGTAACCACA GCCTCGACCA TGCCTGCTCC 200
CTCTGACCCA GCTTCACC 218

25 (2) INFORMATION FOR SEQ ID :528:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :528:

AACCTNATGA CTCTCCATCC CTTGAACCA AACATCTAGC ACTCAGCTCC 50
AGCATATTTT ACCATTCAAC CCGAAATTCA CAAACGCTAC TTGTCGACTT 100
40 GTAACCAATT TACTCAGCAA GTGCTGACTC CTTAACGGAT CATCCCCATC 150

276

CTNCGCTGCA AGGTGACTCA CTAAAATCAT NTGTTAACAC CAACATTATT 200
TTTACACCCA GTGTGTAAGC CAGAAGGGC 229

5 (2) INFORMATION FOR SEQ ID :529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :529:

ATATTATTCA TCATCCCAAG GTCACATCTA GTAAGATGGA AGACTTGGCA 50
ACAAGTGCAG GTTTTGTGCTT TCTTTGATTC ATATCGTGCA AGACTTCTTC 100
20 CTTAGCCTCT TTGCTTC 117

(2) INFORMATION FOR SEQ ID :530:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
30

(xi) SEQUENCE DESCRIPTION: SEQ ID :530:

35 TCGCAGCAGA AGGAAGCTGA TCCACCATCC GGACAACCCG AACCCAAGCT 50
GAAGACGAGA AATGATCCAG AAAGAATGTG CTGCAATCCG GTCATCTTTT 100
AGAGAAGAAG ACAATACACA CCAATGTCGA AATGTGGCAA AATTACTGTA 150
40 TATGCACATG CTGGTGCTAC CCTCTCACT 179

277

(2) INFORMATION FOR SEQ ID :531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :531:

AAAGCATTCA AGTAAGAATA TGGCAATAAA AAACAAAAT ATCTTCTCAG 50
CATTCAAAC AAAACGCATA AGTCATTCCT AACTTNAGAG CTTTATAGCA 100
TTTTCCTAGA CAGGAAGGGA AAAACAGTT AGCATTTAAA AGTCCGAAA 150
GCTTTTTTCGT TGNNTTAATT ACATCAACNN TCTGCCTTTG TCCAAATCCC 200
TTAT 204

(2) INFORMATION FOR SEQ ID :532:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :532:

AAAGGAGCTC AGAACTTCAG CTTGAGCAGG AAGAGGAGGA CGTGCCAGAC 50
CAGGAACAGA GCAGCAGCAT CGAGACCCCA TCAGAGGAGG CGGCCTCTCC 100
CCACAGCTGA GGGGCTGGGC TAGGGGTGGG TGGAGCCCTT TTAAATACC 150
CTTCTTCAA AACTTAGCTC TGAATGGAGA AAC 183

278

(2) INFORMATION FOR SEQ ID :533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :533:

GAAACAAGTT CTCGCTCATC CCTGCATTTC TGCCAACTTC AGCTTGCAAT 50
ATTTATACTC CAGACTATTT TCATCAGACA AAAACCAGTA AGCAGGGTCC 100
TCTTTGAGAA GAGTTCTCTC TTTGGGAGAC AGGCTGCCTT CGATGACACG 150
TTTCACAAGC TGGTTGATGG TGCCCACTAC CCGTGATCTG CTCGCTGGGG 200
GACAGCATCA CTCAGACTAC TTGGAGCCTT GCCTGAATTT CAGGTTTCGT 250
AGGAGGAATA ATTTTCTCCT TCTNTNGTAT CGNCTCT 287

(2) INFORMATION FOR SEQ ID :534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :534:

AGCCACTGCC CCTCTTGTCT ACGTATTCCC AAAATTAAAC TTTGATGCCT 50
GACTTTTTGC AGTCAGTTTT AAGTGAGCTC CCTGAGGTGC CAAGGCCATG 100
GTGTCCCCCT GCTGCGTCTG TTCGTCAGCT GAGTTCTTGT GAATCTNTGT 150

279

TTAG

154

(2) INFORMATION FOR SEQ ID :535:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :535:

15 GATTACCCTA TATCTACAAT TNGAGGTAAA ATAGAAGCAA CACATAAAAG 50
GGCCTATTTT TGCTACCATG TCATATAATT CTCCATAGTG AATATTGTGA 100
TAAAGCTACT GAAAACTATG CCTCACAGAG CCTAGCTTCT TGTAGAGCTG 150
20 GTATTTTACA ACTCGCATTG CTTGGAAATC TCAACACACG TAAGACTCTC 200
CTAGGAAGGC AC 212

25 (2) INFORMATION FOR SEQ ID :536:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :536:

GGAAGCTCAA TGTCCGGCAG GTCAATGCTT CNCGGACACG GATCATT TTT 50
ATCTGATTCC AGCCTGCTTG CAACCCTGGA ATCCTCTTGT TCCCTGCTGC 100
40 CTGCCCCCTTG GGAAGGNA CA GTGATGTCTT TAGGGGAAGG AGGAGCCCCCT 150

280

NTCGGCAGTT GTCTTACT

168

(2) INFORMATION FOR SEQ ID :537:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :537:

15

CGGATCATTT TTATCTGATT CCAGCCTGCT TGCAACCCTG GAATCCTCTT

50

GTTCCCTGCT GCCTGCCCCT TGGGAAGGNA CAGTGATGTC TTTAGGGGAA

100

GGAGGAGCCC CTNTCGGCAG TTGTCTTACT AGGNNNTAA TGAAGTA

147

20

(2) INFORMATION FOR SEQ ID :538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :538:

GTGGAATCTC AATAATGACA CAAGGTACCA ACTGCCAGCA TTTCTGCGAG

50

35

GCAATCCTGC TCTTAATCTG CAAGATGGAC CCTTCTGCAG AGAGATTGCT

100

GTGGGTGATT CTAAGGACAG ATTGTTATAT ACGATGTGGG AGAGCAGATT

150

GCTGTTCCCC GCAATGATGA ATGGGCACGG TTTGGCCGAA CACTTGCAGA

200

40

AATNAATGTA AAGCCNAACT GATGTAGAGA GGACGCAGCT GCCCNAATAC

250

281

(2) INFORMATION FOR SEQ ID :539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :539:

AGAAGGTAAG GGAGTGGGAG GCAGGTGGGT GTTCTGGAGG GGGTATCCTT 50
GTGCTCTAAG GGTGCTATGT TCGATGCTGG TGTTTCGGGG ATGGTGAATG 100
CCCTTCTTTA ANNTTAGAGG GAAATCCAAA CCAATAGGCC CCAAGGTTGC 150
CAGTGGGATA GGGGTGTAAA AAAGTAAATT GGGC 184

20

(2) INFORMATION FOR SEQ ID :540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :540:

AACTTATAGA AAAGTAAAGG AAACCCCAAC ATGCATGCAC TGCCTTGTGA 50
CCAGGGAAGT CACCCACGG CTATGGGAAA TTAGCCCGAG GCTTANCTTT 100
CATCATCATG TCTCCCAGGG NGTGCTTGCA AAGAGATATT CCGCCAAGCC 150
AGAT 154

40

(2) INFORMATION FOR SEQ ID :541:

282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :541:

10

AATTGAATTC TTAAGAAGCT GTCAAATATG GCAGTCTTTT GATGTTAGTA 50
ATTTTGTTTT CTCTGTGTT ATTGGTTCAA AGTACTGGCC TTTTCCTTCA 100
TTTCCAGTAA TTATTTTATA ACTATCACTT TTAATTGAGT GGAAATTAGA 150
TGATTTGGTT ATACTGTGAA ACAGC 175

(2) INFORMATION FOR SEQ ID :542:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :542:

30

AAGTACCTTT TCCTGCAGCT GCCCGTATGC CTGAGTGACT AAGGGGCAGT 50
CGTGAGAGGC AGAGTCCAAG ATCTCATTGG TCGTTTCCAG ACTGCCGTCC 100
AGCCGTGCTG CTTTCATCAGG GCACACTCGC CGCCCTCCTG GGGCCAGGTT 150
GCACATGTAC AGGTACCCGT CGGCGCACCC ACCAACAACG CGGTCTTCTG 200
AATCGCGACT GGCNAACAGA T 221

40

(2) INFORMATION FOR SEQ ID :543:

283

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :543:

AAGTAGATAG CTTGCATCCT GACACCGTGG CAAAGTTAAG AAAGTTGAAG 50
GAGAAACATA CCTTGAGAGG GGGTTTTCTT TAAACTAGT GTTAGAAGCT 100
TAGGGATTTT TTTTTTTATT CCTTACTAAC TTTCACCCAG AACCGCTCTA 150
TTTGACTTGT GCCGACATTG CAACTTTNT GACAGG 186

(2) INFORMATION FOR SEQ ID :544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :544:

AGCATCCTTG CCACCTCCCC ACCCGGGAGT CAAGGGTCGT GGTTCGCT 50
TGAACAGGCC ACAGCCGTAG CTGTAGAGAG GCCAGTGGTA CATCAGCCCA 100
CCGACAGGAG GAGGAGCCCT GGCTTGAGGG AAGGGGAAGC CCAGGCCTGT 150
GCC 153

(2) INFORMATION FOR SEQ ID :545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs

284

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :545:

10	GATTCAGCTC CAGCATCCTT GCCACCTCCC CACCCGGGAG TCAAGGGTCG	50
	TGGTTCTGCC TTGAACAGGC CACAGCCGTA GCTGTAGAGA GGCCAGTGGT	100
	ACATCAGCCC ACCGACAGGA GGAGGAGCCC TGGCTTGAGG GAAGGGGAAG	150
15	CCCAGGCCTG T	161

(2) INFORMATION FOR SEQ ID :546:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :546:

30	AATAGCCCTG AGGTCATCCT GCAAAGTGCG TATCAAAAAA TACGAAGTTA	50
	GGGTGACAAA GTTTGACAGT GATGTTATAC AAGTCAAAC TGAAGGTCA	100
	TAGTAAGCAT ACCTATGCTG AGAGAAAGCA TCAAATCCTT TGTGTACACA	150
35	TTTAGTTTTA TTGTAACAAA GCAACTTGTA CACTTTTA	188

(2) INFORMATION FOR SEQ ID :547:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

285

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :547:

ATNCCTTCTC CATCCANTTA GTTANCAGAA ACTAATCAAA AGAAAGTCTG 50
ACAACTGCAC TCCCCCTTGC ATGCCATTCT CTCAAGCCCA TAATCTTGGA 100
GTATCCACAA CGTGCGAAGG CCTACCCTTT GTGTGTACTC ATCTCACGTT 150
TACGTATTTT GTNGTTGAGG AGCTCCTCTA CAAATGTTGC GTATCTTCCG 200
AATCACTCAT TTAGAAAA 218

(2) INFORMATION FOR SEQ ID :548:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :548:

GGAGGAGACC ATCAGNCCCG TGAAGACCAC TCCTGACGTC TCGTGT 46

30

(2) INFORMATION FOR SEQ ID :549:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :549:

286

AGGGGGCTAA NGGTTGGGGG CAGGAGGCAT TGCTGATGAT CTTGAGGCTG 50
TTGTCATACT TTTCACGGTT CACACCCACG ACGACACGGG GACTCAGCAG 100
5 AGGGGCAAGA CACGACCTTT AGTTTCCCCC TTGCGATAAN CTCNC 146

(2) INFORMATION FOR SEQ ID :550:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :550:

AAATATNGAN TATCCATCCC CTCAAGCATT TATCCTTTGT GTTACAAACA 50
20 ATCCAATTAT ACTCTTTCAG TTATTTTAAC ATGTACAATT AAATTATTAT 100
TGACTCTAGT CACCTTGTTG TCGAGCAAG TACTAGGTCT TATTCATTCT 150
25 TTCTAACTAT TCCAGGCCCT TTTAATCAA GAAGGCTCCC TAGACC AAAA 200
TTTTAAAAAG ACAATGCTAG G 221

(2) INFORMATION FOR SEQ ID :551:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :551:

40

AAACATCGTT TATTCATCCA GCAGTGTTC TCAGCTCCTA CCTCTGTGCC 50

287

AGGGCAGCAT TTTCATATCC AAGATCAATT CCCTCTCTCA GCACAGCCTG 100

GGGAGGGGGT CATTGT 116

5 (2) INFORMATION FOR SEQ ID :552:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :552:

CTCATCCTCT CCTATTACAT AGTGAAGCCC ATGNCAAATA GGAAGAAGCT 50

20 CAGTATCGCT CCTCCCACCA TAACCCCCCT TAATGCCTCC TGAACCATAG 100

TNCCCTCCAC TATATATCCC CCCATGTTCC TGCTACCCCA AGTTTTCACT 150

(2) INFORMATION FOR SEQ ID :553:

25 (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :553:

35 ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT 50

GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG 100

40 GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG 150

NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATAT 189

288

(2) INFORMATION FOR SEQ ID :554:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :554:

ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT 50
15 GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG 100
GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG 150
NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATATG CCTGGAAC 198

20

(2) INFORMATION FOR SEQ ID :555:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
.. (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :555:

CAAGCTGAGG AGCAAGGAGA GCCAGTCTGA GTCCCAAAC TGAAGAACTT 50
35 GAGTCTGATG TTCGAGGGCA GGAAGCACCC AGCACAGGAG AAAGATG 97

(2) INFORMATION FOR SEQ ID :556:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

289

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :556:

TCTGCTGTCT GTCGCAGGAG AAGGAATGTC AGAAACTTCA TCCTCTTGTT 50
GGGGAATGCA CCCTCNTGAG TAGGCTGACC CATGAGGCTG TGGGAATTGA 100
10 GTCTTAGGAC ACAGAGACCA GGGTGTGAA TTTTCTTCCC TGCCCCTAGG 150
CTGTTCAAGGT CTTCTGTCAG CAGTCAGGGC TGCAAGCCCT GGAAAGGCAT 200
15 CAAAAGAGGC CCAGCTCCAG GATCGTGTGT ATGCTCTCCA GCAGACAGCT 250
CTTCAAGGGT GATCTTGTT 269

20 (2) INFORMATION FOR SEQ ID :557:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :557:

ACTCCCTCAA GGTGCGTGGT CTAAGCCTAC AAGAAAGTTT GCCTATCTGG 50
ACCCTGNCTC ACGAGGTTGG CTGGAAGTAC CAGGCAGTGA CAGCCACCCT 100
35 GGAGGAGAAG AGGAAAGAGA AAGCCAAGAT CCACTACCGG AAGAAGAAAC 150
AGCTCATGAG GCTACGAAAC AGGCCGAGAA GAACGTGGAG AAGAAAATTG 200
ACAAATACAA AGGTTCTCAA GACCCACNNA CTCCTAGNTT NAGCC 245

40

(2) INFORMATION FOR SEQ ID :558:

290

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :558:

10

GAATTTAAAA AAAAAGAAAG AAAGAAAGAA AGGTTCCATC TTAGATTCTC	50
ACAACCTTCG TTCCGCAGTT CATTAAATCCG ACTCTGATGC TAAGGTGACA	100
GTGTATGTAA GTAGATTTTT GTTTTCAGTG AAGGAGACCT GGGAAAAGAT	150
GGATTTCTCT CTGTATCTTA AGAGTTATCA GAT	183

15

(2) INFORMATION FOR SEQ ID :559:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :559:

30

GTCATCTTTG GAAAGTGAGA TAACCAAGGA AATAATCGAA GGAGTTAGGG	50
AGATGATTAC GTGATAATGA CTTTGGGCGC TTAACCTTTG ATCCCGGGTA	100
TGCTNAAGAA GCTGAC	116

35

(2) INFORMATION FOR SEQ ID :560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

291

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :560:

CCTTGATGAT ACCATTATCC TCATTATAGA TGATGCACGG GCCCCTGCGC 50
TGGATACGGC GACGGTTTCT CATTTCCTT TGTCAGCTCT CATTGCTGA 100
10 GAGGCATAGA CCTTTTTGAT ATCATCAGGC TTTCCGTTTT TAGGAGCAAA 150
ACAGCTTCTT 160

15 (2) INFORMATION FOR SEQ ID :561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :561:

GCAGTTGGCA GGTGCACTAT CCCAGATGGG CCACTAATAG AAAGTTCCGC 50
AAATGCACCC CGTTCCCCTG TGCGAGATCG TTTGAATNAG ACCAGAACT 100
30 G 101

(2) INFORMATION FOR SEQ ID :562:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

292

(xi) SEQUENCE DESCRIPTION: SEQ ID :562:

ATAAGTTATA GCAAATACAG TCTTCACAGA TTTGAGTAAC TTTATTGAT 50
5 TTTATAGTGA TTTCTTAAGG CCTATATCCA ATGAAACCAT TTCCAAGCTC 100
TATGAGGAGT GGAATTTTAG ATGTCTATTA CATNGTCTT TTAAAAGAAA 150
AATGCTTAAC NNCTAGAATG AGCAAGATTA CTT 183

10

(2) INFORMATION FOR SEQ ID :563:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :563:

AGAGACACGT GAAATTCATA TCTCAAANNC ACAGAGCTGA GACTTTGGGC 50
25 CTAAATACTG TACCACTGGT TCCCTGAACC AAGGAAGAAA AGTGTCGGTA 100
AAGGCCCGTT AAGACAAGAT GGCAAGGAAA AGCACCTTAA ACAATGGTAA 150
GATTTATGTT AGATCAGTGG TAAGAGTTTC TAGTGAC 187

30

(2) INFORMATION FOR SEQ ID :564:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :564:

293

GGGACCCCAA ATCACATCCA GAATACTAGA GTGAGGCAGC TGCAACATGA 50
CACAGAAAAA TGAATCAGG ATTTAGGGGA ATTGGATTTC AGTGCCTATT 100
5 GAGACACGAT CTAGGAAGCC TACCACTTTG GCTGCTCACT GTATGCACAC 150
AACCCNANNA NAATNGATGA AAACAAGAAT GTACAGCATG CTCCTAACAC 200
AANGTGACTA TTC 213

10

(2) INFORMATION FOR SEQ ID :565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :565:

TCCATCTGAC ATCGCATTTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG 50
25 GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTGATGC TATCCCCCAG 100
CCCAATACAA AATACACAGA AAAAGCAATT ATTAAAATAC TGGCTTCGGT 150
TTCTTTTTTTT CCTTTAA 167

30

(2) INFORMATION FOR SEQ ID :566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :566:

294

GAAGATACAG AACCATCCGT GAAAATCATT TAGCACTGGA GACCTTCTTT 50
GTATTACTTC CTNGTTACTA GACCTCTAA TTCAATGGGG CCCTGCTGGT 100
5 TTGTCGATGA ATTGAGCAAC TGAGAACG 128

(2) INFORMATION FOR SEQ ID :567:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :567:

GGAGGCTCGG GAGTAGCATC CTCAGGAGTA GTGTAGCGAG CAAATTTGGA 50
20 AAGTAGTCCT CAATCTTCGA TTTCCAGCA AGGACTTTCT CAGCNAGCGA 100
TCTCGNTTGT TGAGGAACGG ATCAAGAGAT GNNNGTNTAG CTGTNNTGTT 150
25 GTTTAGATGT CTTGAAGAGG TTAGAGCCTC CTGTAGGCGG TTGGNNTGGG 200
NG 202

(2) INFORMATION FOR SEQ ID :568:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :568:

ATGTCATGAT GCCTAACTCA TACACTCTTT GCCTCAAATA TAATTACTAA 50

295

AAACAAATAT AGTATAAACA TTAAACAAAT GAACAATAAT CATCAATAGA 100
CGGGTTACTT TCAAGGAAGA GTTGTTTTGT GACAAATTCT ACTCTTGATC 150
5 TA 152

(2) INFORMATION FOR SEQ ID :569:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :569:

CAGGTCCGCG TGCTCTCCGC ACCACCCAC TTCATTCCGG CCAAACCAAC 50
20 CGCACCCCTG AATTTCTCCG CAAATTCCT GCCGGCAAGG TCCCAGCATT 100
TGAGGGGATG ATGGATTCTG TGTGTTTGAG AGCAACGCCA TTGCCTATTA 150
25 CGCGAGCAAT GAGGAGCTGC GGGGAAGTAC T 181

(2) INFORMATION FOR SEQ ID :570:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :570:

ATCCCTTGGG AGTTTATTCT CCTGGTAAGC TGTAATTGCA TATCCAGTTT 50
40 AACTGGACTG GGCTGTGTTG GGCGAGGATC NGCAGGGTTT TTTCTCNNT 100

296

NGAAAGATGA AATAGATTNT TGAGCACTGG NTGCAGAGCC AAAATGCNTA 150
ATGCTTT 157

5 (2) INFORMATION FOR SEQ ID :571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :571:

GGCACTAAAG CCTTTAATAA TACGAGATGA AATGCAACNG TGNNAATGACA 50
AGTAAGTGAG CCTGACCTGG CATTGCCTCG CCTCACCGCT GGCTTTGACC 100
20 AGGGTATGAT CTTTAACTTT TCTGAGCTGA TTTGATCGTG GTCTTTACAC 150
ACAGGTGGTC GTTCCTGTTT GGACACTGTT TTATTGTTT GAC 193

25 (2) INFORMATION FOR SEQ ID :572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :572:

TCGCAGGAGA AAGAGGTTTT CAGAGGCCCT GAGGACATGG CTGCCCTTGA 50
GAAGGATTTG AGGAGGTTGG TGAATTTGT TGAAGGAGAG GGCGAGGAAG 100
40 AAGGAGAGGA TACTAAAGTT AAAACGTCAC AAGGTGTGCT TTTAAGGGAG 150

297

CTTTCCTGTT TTAAACATGA AAGTGTGGC

179

(2) INFORMATION FOR SEQ ID :573:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :573:

15

AGGACCTCTA AGACATCCTT ATGACGACAG TTTGTCCAA GGGGATATCC

50

ACAGAGTACC TTGTGGCATT AGGTGATTGT AGTCATACAC TTAAAAAGA

100

TTTTATTTCT GATCTTTTGG CGATCTTCTT CTGCCCCATG NNGCTGTTAC

150

20

TTNGCNCGGG NAGCGGTAA TTCTANCCGC TAGGTGTGC

189

(2) INFORMATION FOR SEQ ID :574:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :574:

35

GTGCCTTCTA GGTTTTGAAC TTCTATGCAT TAGCGCAGAT GTGGAATGCG

50

TAAAGGTGTT CATAGTTTGA CTGTTTCTAT GATGTTTTTT CAAAGAATCG

100

TCCTTTTTTG AACTATAATN CCCCNCGGTT ATTTTACCAT CACAGTTTAA

150

40

ATGTATATCT TTTACGTCTC TACTCAGACC ATATTNAAA GGGGCGCCTC

200

298

ATTATGGGGC AGAGAACCTT TTAATAAGTC TCATTAGAT CTGAATTTTG 250
GTTCTAAGCA TT 262

5 (2) INFORMATION FOR SEQ ID :575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :575:

CCAAGGAACC ATCTGCGCCG CAAGCCAGAC CCCACAAGAC CTAGNTTGGT 50
CCTGAC 56

20

(2) INFORMATION FOR SEQ ID :576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :576:

GCGAGTCTCA AAGAGTAGAG GAGCGTCTAC TATCTTTCAA CTCCGATCTT 50
CTGATGNCGG ACTTTACCGT GACAGCGAAG TGGTATTGTA CGTCCAGGCC 100
CGCCAGCCAC TGTCTTCATG CAGGAACCAC AGTGCCAGAT CCCCACAGCT 150
CGTATCTT 158

40

(2) INFORMATION FOR SEQ ID :577:

299

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :577:

10

GGACCTTGAC CCACATCCAT GTTGAGGAAT GTCCTCTTGT CAAGGTCAGG 50

GAACAGCACC CACAGAGGGC CTCTGGGTCC CTCTCTGCTC AACTCCCTCT 100

15

CTCTCGGTTC CTGCGAGGCT CATAGGGTGC AGGGCCCAGC AGAAGGACTG 150

AGTCTTCCTC CTGGACTTCT GGTCTGGTA GGCTGTGCTT CATGCTCTCC 200

TGTCACCTGT ACTGTAAGGA ACTATTATGA CAAACGCATA AAGAATATGA 250

20

CTTTG 255

(2) INFORMATION FOR SEQ ID :578:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :578:

35

GAGGAGTCCA TGCCATCCTT GATGGAAAAG AAAGTGAAGA GAAAAGACAG 50

CCTGTGGAAG AAGCTCAAAG GTTCTTTGAA GAAGAAGAGA GAAAATATGA 100

CATGATATCT TTGCTTTTGA GTTCCTCACG CTCTCTGAAT TTATTAGTTG 150

40

GACAATTCCA TATGCAGCAT TCTGCTTCAA TATANCTCTT NNGGTCTCTC 200

300

TCTCTNNAAT ATTTGCCTGT AGGTAAAAGC AAGCTCTGCA TATCTGTACC 250

TCCTTGAGATA GTTTTGT TTT 270

5 (2) INFORMATION FOR SEQ ID :579:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :579:

GAGTTTTCAG AGGCCCGTGA GGACATGGCT GCCCTTGAGA AGGATTATGA 50

20 GGAGGTTGGG TGGATCTGTT GAAGGAGAGG GNAGAAGAGG AGAGGAATGC 100

TAAAGTTAAA ACGTAATAAA GATGCTGCTC TTACGGAAG 139

(2) INFORMATION FOR SEQ ID :580:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :580:

35 GGCAGGAATA CATATAGTCA TCATTGCCAG ACTTAATATG AGAGGTGAAA 50

TGTTTCGATCC AATTTATTTT TTGGATAAGT TTTTCTTTCC TATNCCTNTN 100

40 GTTTTGATAA TATAATAAAG AAGATGAGGG GCCCA: A TATAGAGCTC 150

CTGAGNGAGT TTTNGGAG 168

301

(2) INFORMATION FOR SEQ ID :581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :581:

CGGAGGGCCC TGT TTGGGAA AAATAGGATT TTAAAAATAT GGTTCATTAA 50
TTTAGGTTTT CTAACATCTA CTTGGGGATG TAGCCTCCAG TGAGGTCAGT 100
TAAGTGGGAC AGAAACGGCA GAGGGAAGAG GTCTTTGCTT CCCCTGGGCC 150
CATTCTCCCT GGCTGCCAGC CCTTGAAGTC AGAACACCAT GGGAAAATTC 200
AGGAGTCGGC ACTGTAGCCG TCAAGTGGCG CTACTTTCCA CA 242

(2) INFORMATION FOR SEQ ID :582:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :582:

GCATTTTTCT TGTGTGCTGT TTATAATAGC AAAGCAG 37

(2) INFORMATION FOR SEQ ID :583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

40

302

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :583:

GGAACAAAGA AAATGTACAG AGTTATATGC GCTTTTTTTT GGTATGGGG 50
ACAAGAAACA CTTACCAACA AAAATATTTC AACAACCCCA AAATAACTTA 100
CTCACAAATA TGCAAATA TCTATGGCAT AGTATTTTCG ACTCGATGAC 150
ATTTAGAGAT AAAAAATCAA ATGGAGCTT 179

15 (2) INFORMATION FOR SEQ ID :584:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :584:

AACTGCCATG AAGTAACCTG AAGGAGGCGC TGACTGGAGG GATTGATTAC 50
AGGATCGGAA CACTCCACAC TCGCCATTCT CTGCATATAC CGGTTAGCGA 100
GGCGAGCCTG GCGCTCTTCT TCGCGCTGAG CTAAAGCTAC ACACAATGCT 150
TTGCGACCAC AATNCACCCT TCATTTCGTA ACTGCT 186

35 (2) INFORMATION FOR SEQ ID :585:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :585:

5 ACCCACGGTA CTTACATCCT ATGATATGGC CTGCAAAC TA AACTACAAAC 50
 GCACTCACAT CGCTATAATC CTTTAAAGGA CTTAAACTTT ACTCCATTAA 100
 GACTTTTATG ACTTCTAACA ACCTCGCCAA CCTCCTCACC CCCCACTATA 150
10 CCTCGGAGAA CTTTCGCGTA ATAACCACGT 180

(2) INFORMATION FOR SEQ ID :586:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 183 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :586:

 ACCGACATCA CGANNGACTT GGTCTTAGTT GAGCAATTTG GCTAANNNNN 50
25 NTNCTNNTTA GCACGTTCTG AGTCTGTGGG ATAGCTGCCA TGAAGTAACC 100
 TGAAGGAGGT GCTGGCTGGT AGGGGTTGAT TACAGGGTTG GGAACACTCG 150
30 AGANTGGCAT CCTGCATATA CTGGTTAGTG AGG 183

(2) INFORMATION FOR SEQ ID :587:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 280 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :587:

304

AGGTCAAGTC TACAGCTGGA GACACCCACT TGGGNGNANG AAGATTTTGN 50
 ACAACCGAAT NGTCAACCAT TTTAATTGCT GAGTTTAAGC GCACNTTAAA 100
 5 GAAGGACATC AGNGAGAACA AGAGAGCTGT AAGACGCCTC CNTACTGCTT 150
 GTGAACGTGC TAAGCGTACC CTCTCTTCCA GCACCCAGGN CAGTATTNAG 200
 NTCGNTCTNT CTATGAAGGA ATCGACTCTN TACTCCATAC CNNNCCGATT 250
 10 GAGACTGATG TGACNTTCCT GGGACTGNCA 280

(2) INFORMATION FOR SEQ ID :588:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :588:

25 GGTGAAGAAA CTCCAGATAT CAAGGAATTG GGAAATCCTG GGCCAAACCA 50
 CCCCAGATG ATTACACTGA AATGTAGTAT TAGTACTNCT GCCAGATCTC 100
 TTTTAAACAT CATGTGCGTC TCTTGGGATC CAGCAAAGT GTTAAGCCAC 150
 30 AATGCCCTTG TGCCTTTTAA TATACCACAG TGCCAGTTAA ACTAATATTT 200
 TTTTTTGTG CTTTTTGGGG TATTTTCATT AGTATTTTCAG CAAATCTCAT 250
 35 GATAAAGGNC AAGGNCAAGA ACTNCAGAGN ACTGAGCAGA GAGGCTNGTG 300
 ATGAAANGTG AAGGCTTCNA CTGACTTTAN GCAGTGGCAG TCANGNTACT 350
 GNGNNGCANG CTTANCTATG A 371

40

(2) INFORMATION FOR SEQ ID :589:

305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :589:

10

GAGAGAGAAC ACTCCCCTCC ATCCCAGCAC TATGCACAGT TCACGGCTCA 50
TATGCAAAGT GGAAGACACG TGGGACAAGA GCAAAGCACA AGTGACACAT 100
GGTCCCTCTC TAACACCTCA GCACACCAAC CCTGACGCTC CCATCACAGA 150
TGCTGNTCAT TCTTNCACGG NCCCCTTTTA TAAT 184

15

(2) INFORMATION FOR SEQ ID :590:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :590:

30

GGGGGCCCCG CGTNCACNCC CCCCACTCT TGGTAGGCAA TGCTTGTCCT 50
NATATAGTTG NNGTCCTATC GAGTGACACT CTCGTTTCATG GATANGGTGN 100
GTAAAACCCN TNGTNGCATC CNNATTGGGN GCANTGNGCC TNTCCCCTTN 150
AANGGTTTTT GCNTNCACTC GACCTNGGGA GGATTCAATG NACNNNCTNG 200
CANTGGNCAA GCNTTGNTTG CNNGNATTGA GAACCCNCCA ATT 243

40

(2) INFORMATION FOR SEQ ID :591:

306

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :591:

10

ATTCGCCCNN TAAGTAAGTC GTNATTANAC GCGACGNCTA CTACTGAGAC 50

NCGCATGCGC TCTCTCTACA CTAAAGCTCG TCGCTNGNTN ACTTGCGNGN 100

15

NAAAAAAACC CCCTGGGNNC GCTTTTCACC CCCAACTTT CAAATTCCGC 150

CCCTTTNGGC NANGCCCAAC CANNCCCCC CCCTTTTINC CGNCCCANNC 200

TTNGGNCNTA ANNATTNAGN CGGNANGNNN GGGCCCCCGG CCAACCC 247

20

(2) INFORMATION FOR SEQ ID :592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :592:

GGAGGGGAGT AGAGGAAATT TTCATTCTGG AAAAAATGC ATACTGTTTG 50

35

ATATATTACT CNTCATGCTT TCCACAGATA TTATACACAG ATATTATATT 100

CCANGGATTA CGTTGCAATG TCTTCAAAA TAGANAATTC ATTTTATATT 150

TCTNGATGAA ATATAATAGT ANCTNNGCTA CTTTGGGAA TGTGACAAAA 200

40

TACTATGATG ATTACAACCTC ATTAAAGCAT AAATNTGCAT GATTTAACNTN 250

307

CATGTTCTT CTATGANCTN CGTGGNATAT AGGCATATTT ATTAATGCTA 300
TTTANGGCNT NNGTGCTTTG TAATGATTCG NCNTTAGGTG AAGGGNTACT 350
5 TTTNTNNTNC TTCNTAGTAG ATTNGNTTNN NTCTTTTAA GAGGANTCNA 400
NTTTCATGNG TAANCATCAT CTTTT 425

(2) INFORMATION FOR SEQ ID :593:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :593:

20

CGCTGCATGC GTCAGCGCNA CGCGACGACA GCGCGCGCGA CGCGCGCGAC 50
GCACAAAANA AATGCATGCC AACACGAANA TATGTGCACA CAAACGCAAA 100
25 CGCGTGTGAA CACATGCGCG CNNGCGGCNC GCGATNCAA GCTGAAATGT 150
GCNNGNCNGT CGTGNGCGNA AATGTGAAAT GAACAAACAA CAATGAATGA 200
ATGAATGTGA AAAAGAGNGN GNTTGAAAAT TNTANAGNNC CCCCCCNTNA 250
30 ANCAAAAAG 258

(2) INFORMATION FOR SEQ ID :594:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

308

(xi) SEQUENCE DESCRIPTION: SEQ ID :594:

5 GACCCTAACA ATATGTACAA AAATATAAAA TGTAATAAAA AAATACAAAC 50
 AAATTTCCCTT TTAAAGTAC TTTAAGAAA AAAAGCAGGG CCTTGAAGT 100
 TTTGGTTCTT TTTTCCTCCC CTGTTGCAA TTCTCATGGT TTGGGTTGGG 150
 TGGTGGAGAG CGCGTGTCAT CTGCGGGTGC CTGCCCACGT GGGCGGGCGG 200
 10 CTCTCTACTC GAAGG 215

(2) INFORMATION FOR SEQ ID :595:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :595:

25 GGGGCTGGTT TGGTCATCCG AGATCATTA AAATGGCTGA CCCTAACAAT 50
 ATGTACAAA ATATAAATG TAAATAAAA ATACAAACAA ATTTCTTTT 100
 TAAAGTACTT TTAAGAAAAA AAGCAGGGCC TTGGAAGTTT TGGTTCTTT 150
 30 TTCCTCCCCT GTTGCAAATT CTCATGGTTT GGGTTGGGTG GTGGAGAGCG 200
 CGTGTCTCT GCGGGTGGCA CTGCCACGGT GGGCGGGCGG GCTCTCTACT 250
 35 CGAAGGTGAC CACGTTTAGA TT 272

(2) INFORMATION FOR SEQ ID :596:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

309

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :596:

GACAAACTGT TGACACCCGG AGGCCTAAAC GAGGATTTC A GCTTCCATTA 50
TGCCCAACTC CAGTCCAACA TCATTGAGGC GATTAATGAG CTGCTAGTGG 100
10 AGCTGGAAGG GACAATGGAG AACATTGCAG CCCAGGCTCT GGAGCACATT 150
CACTCCAATG AGGTGATCAT GACCATTGGC TTCTCCCGAA CAGTAGAGGC 200
15 CTTCTCAAA GAGGCTGCCC GAAAGAGGAA ATTCCATGTC ATTGTAGCAG 250

(2) INFORMATION FOR SEQ ID :597:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :597:

CTGCCAAATA CTTTCTTCAC CAACTCATGA GGAGAGGGAA CATGCTGAGA 50
30 AACTGATGAA GCTGCAGAAC CAACGAGGTG GCCGAATCTT CCTTCAGGAT 100
ATCAAGAAAC CAGACTGTGA TGA CTGGGAG AGCGGGCTGA ATGCAATGAG 150
35 TGTGCATTAC ATTTGGAAAA GATGTGAATC AGTCACTACT GGA ACTGCAC 200
AAACTGGCCA CTGACAAAAA TGACC 225

(2) INFORMATION FOR SEQ ID :598:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs

310

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :598:

10	ACAAAACGCA GATATAAAAA AGTTACAAAG ATTTTATGAT TTTCATTAC	50
	AAAAAAGTC ATTCACATTT TACACTATAC ACGTTATGAT ATAATACAGG	100
	AAAGTATTAT GTGCATTGTA AGAGAAGGAA AATAGAACTA CTAGATCACA	150
15	CGTGTTGTTT TGTGCTCTAA AATACCTAAA GGTGGATTCA TTTAATGCAA	200
	CACCAGGGAC	210

(2) INFORMATION FOR SEQ ID :599:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :599:

30

	AAAGGAGTTG AGTACTGTAA ACGCAGAGCT ACATAGAAAA AACGGGCTTC	50
	AAAAATCTGC ACAGAGGTTT GCTTGAGAAT TTAGCTACAC AAATATGTGT	100
35	AGAAGTGAAA AAAAAA	116

(2) INFORMATION FOR SEQ ID :600:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

311

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :600:

ACAGTGTGTG CCCTGTCAGC TCCGCAAATT GGCAGTCACT ACGTTTGTGC 50
CCCCTGTAAC CTTGTGATCT TCACTGCCAC TAGCGATGAA GTCTTCATTA 100
TGGCCTC 107

(2) INFORMATION FOR SEQ ID :601:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :601:

ACTGCTAGTG AAATTCACAT GACTCACAAT TCCCTTTAGC CAATGTTACC 50
GAAGTCAGTG TCAAGAAAAC TTAACAGAAA AAAAAAAGCA CAGAGTGAGT 100
TCCTACCATA AAAATCCAGG CTGCCCTGTT TCCTAGCTCT AATATAAGCC 150
ATTTTCTTTC CTTAGTGTAC CAA 173

(2) INFORMATION FOR SEQ ID :602:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

312

(xi) SEQUENCE DESCRIPTION: SEQ ID :602:

5 GGAAGAGAAC ACATACACGA GGACCACTAC CTGATGAGGA CAAGAGAGAT 50
GGAANNNGC TGTGGAATTC CTTTCGGCAC CCTGGATGTT AACCCCTGCT 100
CAGGAAAGGG TGCATCTGTC TTCATCATGC CTCTCTCTCC TCCTCCTCCA 150
GCCACCTCCC AAAGGCAGAG CTGCCGCAAC CTGCCTGGCC ATGTGGTGGC 200
10 AAGTACCCAG TAGGAG 216

(2) INFORMATION FOR SEQ ID :603:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :603:

25 GAAAAAACA TCATGACAGC AACTCTCCTA ACCACAAAA TCACATATGT 50
TATCTTTCTT TCAGGACTAA TAATTAATAT TTAAGAGGAA AGCACATCAA 100
TTTCTAGGGC CCTTCTGGG GAAAGGTCA TATAATTTAG CATACATACA 150
30 TATTCAGTGA ATGCATTCAT ATATTACTAT ATAAACACTC TCAGCTACAA 200
TGGTAATATA ATG 213

35

(2) INFORMATION FOR SEQ ID :604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :604:

5 GACATCTGAT CATCTCACTG GACGCCACAG GGGCAAGAGG GTGGTTTCC 50
TGAAGCAGCT GGCTAGTGGC TTATTACTTG TGAAGGACC TCTGGTCTCA 100
ATCGAGTTCC TCTACGAGAA CACACCAGAA ATTTGTCATT GCCACTTCAA 150
10 CAAAATCGAT ATCAGCAATG TAAAAATCCC AAACATCTTA CTGATGCTTA 200
CTTCAAGAAG AAGAGCTGC 219

(2) INFORMATION FOR SEQ ID :605:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :605:

25

AGCGAACACG AGCACAGCGA GCGCACAGAG AGCAGCAGGG AGGGCAGCCA 50
CCGCCGGGAC GCCGGCAGGG GCACGAGAAG GCAAGGAGCG GACACCCGNG 100
30 NNGA 104

(2) INFORMATION FOR SEQ ID :606:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :606:

314

AATAAAGCAT TCTCACAACC TTTGTTGGGT CAATGATTCC TTTTACCAC 50
ANNTACAGAA TCTCCACCAT AGCATCAATA CCAACTCTGA GGAACCTCGC 100
5 ATAATTCTTA ACTACAAAGA TCCTTCAACA CCCGCATTCT TACAATGTCA 150
TCGCCGGAAT TTTGAGTGTT CTTTCAATAA CCTACANTA 189

(2) INFORMATION FOR SEQ ID :607:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :607:

20

GGAAAAGNTC ATTACATAAG CACCAAGNCA TTGATTATGA TCCACCGGAA 50
GAGCTCGTAT TTATCCTTTG CTTTNAATNG AGACCAAGCT AGCCCTGAGT 100
25 AATTTTANNT GGTTCCTAAA ACATATGGCT TATCGTACTC TAAGAAAAAT 150
GCCTTACGCA CATTCTTTN T 171

(2) INFORMATION FOR SEQ ID :608:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :608:

40

GGAAAAGTNC GCATATAGCG TGCNATAATA CTACGNCTAA GGAGAAACAA 50

315

TTTCCTACAC ATAAAGTAGT GAGAACATCA TCCTATAACA GGGAAGTGTG 100
ATTATTTAAA AAACGCAGAA CTTATTTATT TGGCTTTAGA AATAACTGCA 150
5 TACAATGTCA TAAGTCGAAA AGAACTCAAA ATAA 184

(2) INFORMATION FOR SEQ ID :609:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :609:

GGGGACAGCT NNNNNGTTGT TTTGGAGCCT GTTGACTTTG TATTCTCTGC 50
20 CTGTGATTTT CNNTTCTAAA TGAAACTCCA TGTNNNAACC AGGACGAAGN 100
TGAGAAGGAA AACGCCAAAT GCTTTGGTTA TTAGAGNTTA ATAGGNAAGC 150
25 TCTGTTACAC TAGGTGTAGA GTTCCAGAAT GTTCTTTTGT T 191

(2) INFORMATION FOR SEQ ID :610:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :610:

GCAACTGTGC AAACATCCAT CAGTGTGGAG GAATGGTAAA CTTGGTACAT 50
40 GCATGCANTN GNNNCATATT TTTGTGGTTA AGATNNTGAT GTATAGGCAT 100

316

GGAATGTTAT CAAAAGCACA TTAAGTGGTC AAAGCCAGAT ACAGAAGAGT 150

AGGTATGATT TTATAGGNAT AA 172

5 (2) INFORMATION FOR SEQ ID :611:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :611:

TCCACCTTAC AGACCTGATT TGGCTGCTTC TGACGTCTGT TTCCTAATCT 50

T 51

20

(2) INFORMATION FOR SEQ ID :612:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :612:

CGCCTGAAAC TTTGAGGATA AACTTTTTCA AAAAAATAAA ACAGTATCTC 50

35

TTAATCACTG 60

(2) INFORMATION FOR SEQ ID :613:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

317

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :613:

TTGAAGCTGG GAGGCAGAGG TTGCAGCGTG CAGAGTCGTG CCACTGCACT 50

CCTGGGCGCA CAGCGAGACT GTCTC 75

10

(2) INFORMATION FOR SEQ ID :614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :614:

ACGGGATTCT CTTCTTCGGC CGCCA 25

25 (2) INFORMATION FOR SEQ ID :615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :615:

GCAGTGTA CT ATGTTTCGCAT CTGTGAATAG CCACTGCACT CTAGCCTGGA 50

TAATATAGTG AGAACCCATC TC 72

40

(2) INFORMATION FOR SEQ ID :616:

318

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :616:

10

TCTAACTGAT TTCAAAGCAA ACTCTCTCTT AATTAGGCTG CCTCTCCAGG 50

GGAAATTTAG TGGCAGGGTC CCAGTGAGCC TGTAAGAAGT GTTCTACTCA 100

15

CCAGAGTCAC TACTCCAGGT TGAGGACATG AGGCAGG 137

(2) INFORMATION FOR SEQ ID :617:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :617:

GCAGGGCAGT CTTGGTGTGC AGCCCCTCTC CTCTCTGTCC CCTGACACTC 50

30

CACAGTGTGC CTGCAACCCA AGTGGCCTTA TCCGTGCAGT GGTGGCAGTT 100

CAGAAATAAA GGGCCCATTG GAGGGATGAC CGCATTAC 139

35

(2) INFORMATION FOR SEQ ID :618:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :618:

5 TCTTCTTACT ACACTGGAAG TCTGAACTGG GTGCCTGTTA CCGTCGAGGG 50
TTACTGGCAG ATCACCGTGG ACAGCATCAC CATGAACGGA GAGGCCATCG 100
CCTNCNCTGA GGNCNGCCAG GCCATTGTTG ACACCNNCAC CTCTCNNCTG 150
10 ANNNNCCCAA CCAGCCCCAT TNCCAACA 178

(2) INFORMATION FOR SEQ ID :619:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :619:

ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC 50
25 TTCTGCGGCC GCCACGCGT GGA 73

(2) INFORMATION FOR SEQ ID :620:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :620:

40 TGCCTTACAC ACTCAGGGAG ACCTCGGGTT GTACCTAGGC CTAGTGGACA 50
AACTTTGGTA GAGGGTTCGG TACGACTTAC GACACCTGGC CCTACGTCAT 100

320

AGTCCGTACC CTCAGTAACA GTGTAGTAGC TCTTCCTGT

139

(2) INFORMATION FOR SEQ ID :621:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :621:

15 TTCAAAAACA ACTTTATTCA TGACACATAT TAANNNAAAA CCCCACCCCT 50
GGAAATGAGC TAAAAAATA AACAAATCC ACCTCCCACC TCCCTGNNCC 100
CACTTCCTCC CATGCCCTCC AAA 123

20

(2) INFORMATION FOR SEQ ID :622:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :622:

CACCCAAGAC CATCCTTTAT TGTAGTATTA GTTCATGGTA ACTGCATGAA 50
35 AAAACATTTC NNGAGGAATT TTCAATTTCC AGCTTAAAGA ACNNNCCCAC 100
CAACATAACC AATTTATGAA ANNNAATTCA TTAAAGGTA TAGAACCTCT 150
TGTNNNCATG ATGGCAAGGG ACA 173

40

(2) INFORMATION FOR SEQ ID :623:

321

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :623:

10

TTTATTGTAT CATGAGGCAT TGAAACATCT GAATAAATCA ATGTCTGGGC 50

GGTGAAGGCA GCTGCTTTCT CCTTCACTTC TTTGGGTTAC TAGAGCAACT 100

15

TGTCAGTAGA TT 112

(2) INFORMATION FOR SEQ ID :624:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :624:

ACTCCTTCTG CCCCCGTTCT TCTAGTGAGA GGGGCGGACA AGGGGGCGGC 50

30

GAAAAGAGGA GAAAGGAGAG AAACAAGAGT CGAGGGGGAC AGGGGAGTCG 100

AGGTCTGCAT CCCCTCCCC 119

35

(2) INFORMATION FOR SEQ ID :625:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :625:

AACAGCACGG AGATTGCGTT TATATATCAG ACCAAGCTC

39

5

(2) INFORMATION FOR SEQ ID :626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :626:

CCAGCGCCGA GGTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA

50

20

ATAAAAATCT GAAAACATCC CC

72

(2) INFORMATION FOR SEQ ID :627:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :627:

CCTCCGCCGG AGCTATCTGC ACTACATCCG CAAGTACAAC CGTCTTCGAG

50

35

AAGCGCCACA AGAACATGTC TGTACACCTG TCCCCCTGCT TCAGGGACGT

100

CCAGATCGGT GACATCGTCA CAGTGGGCGA GTGCGGCCTC TAGACAAGAC

150

40

AGT

153

(2) INFORMATION FOR SEQ ID :628:

323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :628:

AAAAGAAGTA GGTCTGTGTCG TTCTGGTTGC CCTAAGAGAA GAAGANNNCG 50
GTGGCCACCT CGAGGTTAAG AGGGATATCA CTCAGCATAA TGTTAAGTGA 100
CCGGCAGC 108

(2) INFORMATION FOR SEQ ID :629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :629:

TCGCACCACT AGAAANCACC GTGACTGAGA AGAATGATGT GACCTTCAGA 50
CTTGACCCNN GGACAATGNC AGCTCCCAAT GNCCGTCTAG TGGCA 95

(2) INFORMATION FOR SEQ ID :630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

324

(xi) SEQUENCE DESCRIPTION: SEQ ID :630:

CCAGCNCCGA AAAGCCAAGA CTTTCATCAAC TACATAGGTC TTACCATTGA 50
5 CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT 100
AGAAAGGCAT CTTTCGCCAG TGGATTGCC TCAAGGTTG 139

(2) INFORMATION FOR SEQ ID :631:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :631:

20

CCACCGCCCC GAGCGAATGT AACCCGGCCT TGGACGACCC GACGCCGGAC 50
TACATGAACC TGCTGGGCAT GATCTTCAGC ATGTNCNNCC TCATGCTTAA 100
25 GCTGAAGTGG TGTGCTT 117

(2) INFORMATION FOR SEQ ID :632:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :632:

CCAGCNCCGA AAAGCCAAGA CTTTCATGAAC TACATAGGTC TTACCATTGA 50
40 CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT 100

325

AGAAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTTGA GGCCGCCATT 150

GGAAGATGAA A 161

5 (2) INFORMATION FOR SEQ ID :633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :633:

CCTGCNCCGA CGATGCCCAG AATCCAGAAC TTTGTCTATC ACTCTCCCCA 50

ACAACCTAGA TGTGAAAACA GAATAAACTT CACCCAGAAA AACAAAC 97

20

(2) INFORMATION FOR SEQ ID :634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :634:

CCAGCNCCGA AGCATTGGAT GCTTGACAAA CTAACGGGTG TATTTGCACC 50

35 TCGTCCATCG ACAGGTCCCC AGAAGCTGAG GGAATGTCTT TCCTCTGATC 100

TTCTTCCTCA GGAATAGACT CAAGTATGCG TTGACTGGAG ATGAGGTAAA 150

GAAGATATGT ATGCAACGTT CATTCAAA 178

40

(2) INFORMATION FOR SEQ ID :635:

326

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :635:

10

CCTGCNCCGA TGCACCCGCC ATCCAGCCTG TCCTTTGGAC CACGCCACCC 50

CTCCAGCATG GTCACCGCCA TGGGTTAGAN CCCTGCTCGA 90

15

(2) INFORMATION FOR SEQ ID :636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :636:

CAGGAGACAC AGACAATAGT CACTACATCA CAGCCTTGTT CTTTCCGAAG 50

GATAAAATGT CATTCAAGAA TGGGGTGAGG TGGTTAGAGG GACTAGGTAC 100

30

T 101

(2) INFORMATION FOR SEQ ID :637:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

327

(xi) SEQUENCE DESCRIPTION: SEQ ID :637:

CCGAGCACGA GACCCTGATG CACATTCTAA AATAAAAGAA TGATGCACAT 50
5 TTTAATAAAG CACAGCACAA 70

(2) INFORMATION FOR SEQ ID :638:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :638:

CCGAGCANAN TCTAACCCGG CCTTGGACGA CCCGACGCCG GACTACATGA 50
20 ACCTGCTGGG CATGATCTTC AGCATGTGCG GCCTCATGCT TAAGCTGAAG 100
TGGTGTGCTT GGGTCGCTGT CTACTGCTCC TTCATCAGCT TTGCCAACTC 150
25 TCGGAGCTCG 160

(2) INFORMATION FOR SEQ ID :639:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
35

(xi) SEQUENCE DESCRIPTION: SEQ ID :639:

CCGAACAAAT GTACGGAATG TGTGAGTCCC TCTGGAGCCC AACATGGATC 50
40 CGGATCACCT GTTTGAAACC ATCTCCCAAG CCATGCTGAA TGCTGTGGGC 100

328

CGGGATGCAT GTGCAGGCAT GGAGTCATTG TCACATCA

138

(2) INFORMATION FOR SEQ ID :640:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :640:

15 CCGACCACCC CTCCTTTTC TTCGTCCATC CAGCACAGCA AGACCAACGG 50

GATTCTCTTC TCGGCCGCC ACCGCGTGGA 80

(2) INFORMATION FOR SEQ ID :641:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :641:

30

AACTAAACTG TTACCTTCCC TCGCTCCACA GAAGAAGACA GCCAGCTTCA 50

GGGGTCCCTG TTGCTGGCCA AGCCAGTGAG CCTGCTGGGA GGCTGGTCCA 100

35

(2) INFORMATION FOR SEQ ID :642:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :642:

5 AGAGGACAGA AAGGAACAGA ATGATCTTCC TACNCACAAC ACAAACGTCA 50
GTTAATGTTC CATCCATGCT GCTTAA 77

(2) INFORMATION FOR SEQ ID :643:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :643:

20 CCAGCGCCGA GAGCAGCCCC AGTAGCAGCN CATGGCCGGG TCCAACGCCT 50
ACATCGACAA CCTTCATGGC GGACGGGACC TGTCAGGACN GGCCATCGTG 100
GGCTACAAGG ACTCGCCCTC CGTCTGG 127

(2) INFORMATION FOR SEQ ID :644:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :644:

35 GTAGCCAGAC CACAACACCG AGTTGTACCC AGATAGCTGG GATTGGAAGT 50
40 GAGGAGGTTT CTCACCCAC AGATAACCCA AGACACAAAT GTGCAATTAA 100
AAGTTTATTT TAGACC 116

330

(2) INFORMATION FOR SEQ ID :645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :645:

CCACCACCCG ATTCGTGACC AAGAAGGCTC TGTGCATTCG GGTTTTCCAG 50
GAGACTCAAA AGCCGAAGAA GCGAAGAAGA GCCTTAAAGG CTGCAGCAGC 100
CAGAAAAACA AGCAAAGGAG GAACCCAGAC AGCCCTGCAA AGCATAACAAG 150
ACACTCAAGA CAGCAATTAA TCTGTCATCA TT 182

20

(2) INFORMATION FOR SEQ ID :646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :646:

CCAGCGCCGA GGTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA 50
ATAAAAATCT GAAAAC 66

35

(2) INFORMATION FOR SEQ ID :647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

40

331

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :647:

CAAGACAATA GTCACATCAT CGCAGCCTTG TTCTTTCCGA AGGATAAAAT 50

GTCATTCAAG AATGGGGTGA GGTGGTTAGA GGGAGTAGGT ACT 93

10

(2) INFORMATION FOR SEQ ID :648:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 114 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :648:

CCCCTTTTTG TCCCCACTGA GATGTATGAA GGTTTTGGTC TCCCTGGGAG 50

25

TGGGTGGAGG CAGCCAGGGC TTACCTGTAC ACTGACTTGA GACCAGTTGA 100

AAAGTGCACA CCTT 114

30

(2) INFORMATION FOR SEQ ID :649:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 81 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :649:

CTGCNCCGAC CACCCCTTCC TTTTCTTCAT CCAGCACAGC AAGACCAACG 50

332

GGATTCTCTT CTGCGGCCGC CACCGCGTGG A

81

(2) INFORMATION FOR SEQ ID :650:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :650:

15 AGGAGCNCCG ACAAAGACA CATTGGACCT GTCAGCTCCT CTGTTTCACC 50
AAGCAGACAC AATAACCTTA CCAACAAAGC AGAGTAAGCC AAGTGCCTCT 100
20 GTGTGACACC ACCGCATNNT GATGACGCAT AATAAAAATA TAACTAATTT 150
AGACTAGAG 159

(2) INFORMATION FOR SEQ ID :651:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :651:

35 CCGACCACCC CTCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50
CTCTTCTGCG GCCGCCACCG CTGGAGCT 78

(2) INFORMATION FOR SEQ ID :652:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs

333

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :652:

10	CCGACAGACG GTCATTGATT ACAACGGGGA ACGCACGCTG GATGGTTTTA	50
	AGAAATTCCT GGAGAGCGGT GGCCAGGATG GGGCAGGGGA TGATGACGAT	100
	CTCGAGGACC TGGAAGAAGC AGAGGAGCCA GACATGGAGG AAGACNATGA	150
15	TCAGAAAGCT GTGAAAGATG AACTGTAATA CGCAAAGCCA GACCCGGG	198

(2) INFORMATION FOR SEQ ID :653:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 224 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :653:

30	CCGAAAAGCC AAGACTTCAT GAACTACATA GGTCTTACCA TTGACCTAAG	50
	ATCAATCTGA ACTATCTTAG CCCAGTCAGG GAGCTCTGCT TCCTAGAAAG	100
	GCATCTTTTCG CCAGTGGATT CGCCTCAAGG TTGAGGCCGC CATTGGAAGA	150
35	TGAAAAATTG CACTCCCTTG GTGTAGACAA TACCAGTTCC ATTGGTGTG	200
	TTGCTATAAT AACACTTTTC TTTT	224

(2) INFORMATION FOR SEQ ID :654:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 base pairs

334

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :654:

CCGCCTCAGA CTCTGGACCA GCCACTGTCC CAGAAGCCAG GCCGGGCAGT 50
10 GGCCTTCTCC ACTCCCCTCT GACTTCTCCA AGGGGCTCAG TGGCCAGTGC 100
CCCCCAGGAG GCTCCACCCT CAACTCAACC CAAGCAAGAG GGACAGATGA 150
15 AAAACAAAAT CCAATCAGGG CGATAAATGG CGGGGGGTTT AATTGGTTT 200
CTGAGCGCAT AAAGCTAAGG AGGGGT 226

(2) INFORMATION FOR SEQ ID :655:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :655:

30

TTAAAAAAT TCCCCCTTT AATTGACCAA AGTAAAGCCA TGACATTTC 50
TTTGGTAACC TGTTTAGAAT TATAAAATC ATTTCATTTG GCCCAGCCCA 100
35 TACGCCCAAG AGAAACTTC CAGACTTTTC TGATGCCATC CAGTTTTGTT 150
CTTACAAAAT GCATATT 167

(2) INFORMATION FOR SEQ ID :656:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs

335

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :656:

CCACCCCTTC CTTTCTTCA TCCAGCACAG CAAGACCAAC GGGATTCTCT 50

10 TCTGCGGCCG CCACCGCGTG GA 72

(2) INFORMATION FOR SEQ ID :657:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :657:

25 AGAGGGTTTT CTATATGTAA TTCTTTTATT CTGTAAAAGG TAACAAAATA 50

TACAGAACAA AAAAATTTC CCTTTTAAA ACTAATGTTA CAAATCTGTA 100

TTATCACTTG TATATAAATA GTATATAGCT GATCATTAAAT AAGGTGTATA 150

30 GTACAATGTA TTCTAAAACT GTTCCGCC 178

(2) INFORMATION FOR SEQ ID :658:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

336

(xi) SEQUENCE DESCRIPTION: SEQ ID :658:

CCGACCACCC CTCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50
5 CTCTTCTGCG GCCGCCACCG CGTGGA 76

(2) INFORMATION FOR SEQ ID :659:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :659:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT 50
20 AACAAAAACC NTGAAAAC 68

(2) INFORMATION FOR SEQ ID :660:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 30

(xi) SEQUENCE DESCRIPTION: SEQ ID :660:

35 CCCAACTTC TTAAAAATC AAGTAATGTT TACAAGAAAG AATAAAATCT 50
TAATCCTTTT CACTTTTAAA GACAATCAGA TAAGATTACC CACTGCGATT 100
AAACACTGAT CAAACTCAGT TGTCTTACG TTAGCATTAC TCTGTCATAG 150
40 C 151

337

(2) INFORMATION FOR SEQ ID :661:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :661:

AGGCACTGAC CCCTGCCACC CCTCACTGCA TTAACCTCAG CCACGTCTCC 50
15 TCCTTCCTCT GCGCTTCCAG TGATAAGGGT ACTGTCCATA TCTTTGCTCT 100
CAAGGATACC CGCCTCAACC GCCGCTCCGG CCTGGCTCGC GTGGGCAAGG 150
TGGGGCCTAT GATTGGGCAG TACGTGGACT CTCAGTGGAG CCTGGCGAGC 200
20 TTCACTGTGC CTGCTGAGTC AGCTTGCATC TCGCCTTCG GTGCG 245

(2) INFORMATION FOR SEQ ID :662:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :662:

35 GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50
AATAAAAACM TGAAAACACC CC 72

(2) INFORMATION FOR SEQ ID :663:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs

338

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :663:

GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC 50
10 AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :664:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :664:

GCCTGCGCCG ACAAACAAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCCGA 50
25 GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC 100
CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG 150
30 CGCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG 200
CGGATAGTCA CACTCCCTGC CGA 223

35

(2) INFORMATION FOR SEQ ID :665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

339

(xi) SEQUENCE DESCRIPTION: SEQ ID :665:

5 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50
AATAAAAATC TGAAAACACC 70

(2) INFORMATION FOR SEQ ID :666:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :666:

20 GCCAGCGCCG ACCGCCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50
TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAAA CCAACCACC 100
TTTCTACGTA CCGTATAG 118

25

(2) INFORMATION FOR SEQ ID :667:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :667:

40 GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTTGCCTAT CACTCTCCCC 50
AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :668:

340

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :668:

10

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTTGATCTTC AACTCTGCAT 50
ACAAGCAGA 59

15

(2) INFORMATION FOR SEQ ID :669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :669:

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA 50
CATGGATCCG GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG 100
CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150
GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC 200
CTGCTCCCAG AGCCCACTTT TTT 223

30

35

(2) INFORMATION FOR SEQ ID :670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

40

341

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :670:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC

37

(2) INFORMATION FOR SEQ ID :671:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :671:

20

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC

37

(2) INFORMATION FOR SEQ ID :672:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :672:

35

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTCGATCTTC AACTCTGCAT

50

ACAAGCAGA

59

(2) INFORMATION FOR SEQ ID :673:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

342

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :673:

10	GCCTGCGCCG ANGCAATCCC TTTGACCTGA GTCTGCAGCA GGTCCCTTTT	50
	GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGGG	100
	GTGAGGGGGT TACCCCTTCC CAGTGTTTTT TATTTCGTG GGGCTCACCC	150
15	CAAAGTATTA AAAGCAACTT TGCAATT	177

(2) INFORMATION FOR SEQ ID :674:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :674:

30	GCCTGCGCCG AGCACAAGAC AATGACGAAC ATTTTAAAAA AAAAGAATGA	50
	CGCACATTTT AATAAAGCAC AGCACAA	77

(2) INFORMATION FOR SEQ ID :675:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

343

(xi) SEQUENCE DESCRIPTION: SEQ ID :675:

50
GCCAGCGCCG ACACCCAGAG ACTACAGTAC TTAGGGGTTA CACACAACAG
5 CCGTAACTGG CGGCTATCTG TTCATAACAA ACAAACCATA GCATATTTAC 100
ACCGCATCAC ATCGAGTGAT TATAGAAATC CATAACACA CCGATTGCAT 150
AAAATCTTTT TTTAGGAAAA AAACAC 176
10

(2) INFORMATION FOR SEQ ID :676:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :676:

50
GCCAGCGCCG ACGCCCAGAG AATACAGTAC TTAGGGGTTA CACACAACAG
25 CCGTAACTGG CGGCTATCTG CTCATAACAA ACAAACCACA GCATATCTAT 100
ACCGTATCAC ATCGAGTGAT TATAGAAATC CACAGAGAGA C 141

(2) INFORMATION FOR SEQ ID :677:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :677:

40

CTCTGAACAG ACACGAAGCT GCCCCTCGTA CAGCCACTCG GGCGCTGACC 50

344

ACCAGGGAAG GCAAAGGCAT AGGACTTCCA CACAGTCCAG AACTGTCACG 100
 CTGACAAGCG CCTCCGCGGC GGCTGCGAGC CGGACTCAGG CGGATCTTGA 150
 5 CAGCCTTGCC CGCGAGTGCC CGGGGATAGA ACCCGTGCGC GTGGACCTAG 200
 GTGACTGGGA GGCCACCAAG CAGGCACTGG GCAGCGTGGG CCCC GTGGAC 250
 CTGCTGGAGA ACAACACCAC CGTCGCCCTG CCGCAGCCCT TCCAGGAGGT 300
 10 CACCAAGGAG GCCTTCGACA GATCCTTTGA GGTGAGCTTG CGTGCGATCA 350
 TCCAGGTGCT GTAGA 365

15 (2) INFORMATION FOR SEQ ID :678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :678:

GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC 50
 CAGGGAAGGC AAAGGCATAG GACTTCTGCA CGGTCCAGAC CCATGTACGC 100
 30 GACGGGCGCC TNCGCGGTGG CTGCGAGCCG GATTCAGGCA GATCTTGACA 150
 GCCTTGCCCCG CGAGTGCCCCG GGGATAGAAC CCGTGTGCGT GGACCTNGGG 200
 TGA CTGGGGAG GCCACCAAGC AGGCACTGGG GTAGCATGGG CCCC GCGGAC 250
 CTGCCGGAGA ACAATACCAC CGCCGCCTNT GCCGCAGTCT TTCCCGGAGG 300
 TCACCAAGGA GGCCTNTTGA TAGATCTTTT GAGGTGAGCT TGCGTGCGGT 350
 40 CATCTAGGTG CTGTAG 366

345

(2) INFORMATION FOR SEQ ID :679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :679:

GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC 50
CAGGGAAGGC AAAGGCATAG GCCAGCACCG ATGAATTCCC TTTGACCTAA 100
GTCTGCAGCA GGCCCCTTTT GCGCTTCCTT CCCCTCAGGC AGCCTCTCTC 150
CCCCCGGGCC ACTCCCGGGG GCGAGGGGGT TACCCCTTTC CCAGTGCTTT 200
TTATTCCCGC GGGGCTCACC CCAAAGCATT AAAAGCAGCT TTGCAATTCC 250
TTG 253

25

(2) INFORMATION FOR SEQ ID :680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :680:

GCCAGCGCCG AGGCTTCTCC TAGGGCTGCT CCTGGGCCTA GCTCTTACAG 50
GCTCGTCCCC CAGGCCTGCC CTTCTCCACT GCCCCCTCCC GTGCCTGGGC 100
CCACACACCC TTCAGGAAGG GGGAGCACTG AGAAGCACAG CACAGGGGCT 150

40

346

CAGCCTGGGA TCCGGTGACG GCCTAGGCAG AGGCTGGGCC AGGAGTCCCA 200

AAGGTCAGTG ACAGTTTCTC AGAAGGGGCC CAGCGTCCAC CTCTCTCCCA 250

5 GGACCAGACA CCCCTTCCAG GCTCCCCCAC CCCCTACGG GCTC 294

(2) INFORMATION FOR SEQ ID :681:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 268 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :681:

CCGCCAAGTG ACACCAAAGC CCTGGTTGAC TTTGACAGCC CCGTGGGGCG 50

20

GCGGGAGGCC GGGCACTCTA GGGTCTACCT ACCAGTGCAA TCGTTTAGCG 100

CTTTTTCAGT GGGGCAGGGC AGGAAGCAGG CGGGACCAGG CAGCCAGTTC 150

25

TCAAAGGCTG CGGGGCCAAC TAGAGGCCAC AGCCCCTCAC CCCTAGACAC 200

TGCCAACCAG AACTGACACG CGACCTCCTG GGCCTGACG CCATTAAAC 250

CAACGTTGGC GCCCGGCG 268

30

(2) INFORMATION FOR SEQ ID :682:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :682:

347

5 GCCACCGCCG AGGAAAACCG TGCCTGTTA GCCATGATCA ACCCCACCGT 50
 GCTCTTCGAC ATTGACATCG ACGGCTGAGC CCTTGACCTA GTCTCCTTTG 100
 AGCTGTTTGC AGACAAGGTC CCAAAGACAG CAGAAAATTT TCGTGCTCTA 150
 AGCACTGGAG AGAAAGGATT TGGTTATAAG GGTTCCCTGCT TTCACAGAAT 200
 TATTCCAGGG TTTATGCGCC AGGGTGGTGA CTTCACACGC CATAATGGCA 250
10 CTGGTGGCAA GTCCATCCAT GGGGAGAAAT TTGAAGACGA GAACTTCATC 300
 CTAAAGCATA CGGGCCCTGG CATCTTGCCC ATGGCAAATG CTGATCCTGA 350
15 TACA 354

(2) INFORMATION FOR SEQ ID :683:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :683:

 CCTCTCCGTG AGGACAGGGC AGTCTTGGTG CGCAGCCCCT CTCCTCTCTG 50
30 TCCCCTGACA CTCCACAGTG CGCCTGCAAC CCAGGCGGCC TTATCCGCGC 100
 AGTGGCGGCA GTTCAGAAAT AAAGGGCCCA TTTGCGGGAT GCCGCATT 148

35

(2) INFORMATION FOR SEQ ID :684:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

348

(xi) SEQUENCE DESCRIPTION: SEQ ID :684:

5	AGCACCGAGG CGCTCAAGGT CCTGGGGAAC CCCAAGAGCG ACGAGACGAA	50
	CGCGAAGGCG CTGGACTTTG AGCACTTTCT GCCCATGCTG CAGACAGTGG	100
	CCAAGAACAA GGACCAGGGC ACCTATGAGG ATTATGCCGA AGGACTTCGG	150
10	GCGCTTGACA AGGAAGGAAA TGGCACCGTC ATGGGCGCTG AAACCCGGCA	200
	TGCTCTTGCC ACACTGGGCG AGAAGACGAC AGAGGAAGAA GCAGAGACGC	250
	TGGCGGCAGG GCATGAGGAC AGCAATGGTT GCATCAACTA CGAAGCATTT	300
15	GTGAGGC	307

(2) INFORMATION FOR SEQ ID :685:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 174 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :685:

30	CCATCTCAAG GCGATCCATG GAAAGCTTCC TGGGGAACGT ATGCTAGCAG	50
	AGCTTCTCCC CGTGAATCAC ATGCCGGAGA TCCCACTCTT AGCTGGCAAA	100
	TGAATCCGAA TTGACACAGC AGCCCCATAA GCATCAGCCC TGTAGAGTGA	150
35	GGAGCCATCT CTAGCGGGCC CTTC	174

(2) INFORMATION FOR SEQ ID :686:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 106 base pairs
	(B) TYPE: nucleic acid

349

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :686:

ACATGCCAAA GAAAGCGTGC ATATTAGCCT ATAGAACCAC AGTAATCACA 50

10 CTAGAGAAAT TCCACTGCTA CAATAAATG TAATCGGAAG CATCTTTACT 100

TATAAA 106

15 (2) INFORMATION FOR SEQ ID :687:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :687:

CAGATTTTTT TCAATTCTCC ACCCGCCAAA AGGGGAAGGG CTTTCCCCCA 50

GAGAAAAGGA AAGGGGGGAA AAGGGGAAAA AACCCAACCC AAAACCA 97

30

(2) INFORMATION FOR SEQ ID :688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :688:

350

GCCTCTCTCT GGGCAAGTTC ATGGCTTCTG TGAGCCCTTT NACTGACCTC 50
CAGACACTGT TAGGCTGGAG CCTCGGTAGC CGTTCCTCCT GCCCACTGGA 100
5 CCTTCCAACA GGCCCTCCTC CCCTCCTTGA ACCGGCCCTT CCTGGCCTTT 150
GAATAGAGTC TAAGCGAACG AC 172

(2) INFORMATION FOR SEQ ID :689:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :689:

20

GCCACCGCCG AGCTCACCCC TGCGGTGCAC GCCTTCCTTG GACAAGTTTT 50
TGGCTTCTGC GAGCCTTTTA CTGACCTCCA AACGCTGTTA AGCCGGAGCC 100
25 TCGGTAGCCG TTCCTCCTGC CCACTGGACN TCCCAACGGG CCCTCCTCCC 150
CTCCTTGAAC CAGCCCTTCC TGGCCTTTGA ATAAAGTTTA AGCGAGTAGC 200

(2) INFORMATION FOR SEQ ID :690:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :690:

40

GCCACCGCCG AGCAGCAGCT TACAGCCAGG GCAGCTTTGA ATGCGGCCCA 50

351

ACACAAATTC ACAAGTGNTC TCAAAAAACT C

81

(2) INFORMATION FOR SEQ ID :691:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :691:

15

TTCCTAACCG ATCGAATGAA GGATTCAAAA TTAACCACTC CAAGGGGGGA

50

TTGAAGGAAG AACCACTCTT AACGGACAAA AAGAAAGAAA GGGGAGGGAG

100

TAACAGGGAT ATGAGCTCTA GCCGCCCAAG CTAGCAATGG CAACCCTTCT

150

20

GGGTCCCCTT TCAGCATGCG GAAGCTTTTC TTCGACTTCA CTCCATAAAC

200

AGCTGACGCT CAAAAG

217

25

(2) INFORMATION FOR SEQ ID :692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :692:

CGGCCTTCTG GAAACCCATG AAAAAAAAAA GTTCCGCACC TCCAAGGGGA

50

GAAGAGTAAG AGACAGCTTT CA

72

40

(2) INFORMATION FOR SEQ ID :693:

352

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :693:

10

TCTGCTGCCG	CCCGCAAGCA	GAGGGACTCG	GAGATCATGC	AGGGGAAGCA	50
GAAAAAGGCA	AACAAGAAGA	AGGAGGAACC	CAAGCAGCTT	TGCGGCTTCG	100
CGTCCAACCC	TCTTGCCCTT	CACCTACGCG	CCTAGAGCCA	GTCCCACCAC	150
GCTCGCGTTT	CCTCCTGTAG	CGCTCACAGG	CCCCAGCACC	GATGGCATTG	200
CCTTTGACCT	AAGCCTACAG	CAGGCCCTT	TTGTGCTTCC	TTCCCCTCAG	250
GCAGCCTCTT	TCCCCCTGGG	CCACTCCCGG	GGGTGAGGGG	GTTGTCCTTC	300
CCGATGCTTT	TTGTTACCGT	GGGGTTTGC			329

25

(2) INFORMATION FOR SEQ ID :694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :694:

TCTGCTGCCG	CCCGCAAGCA	GAGGGACTCG	GAGATCATGG	CCTGCGCCGA	50
ACAAATGTAC	GGAATGCGTG	AGTCCCTCTG	GGAGGCCGAA	CACGGATCCG	100
GATCACCTGT	TTGAAACCAT	CTCCCAAGCC	ATGCTGAATG	CTGCGGACCA	150

40

353

GGATGCAGTG TCAGGCATGG GAGTCATTGC CCACATCATC GAGAAGGACA 200
AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC CTGTTCCCAG 250
5 AGCCCACTTT TTTTTTTTTT TTGGAAATAA AATAGCCTAT CTTTCG 296

(2) INFORMATION FOR SEQ ID :695:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :695:

GCCAGCACCG ACCTAGCCTA AGCCGTCTAG AACCACCTAA GCCCCTAAGG 50
20 AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCGCAGAGG 100
CGTGTCTTAG CACTAACCTC CTCCCTAGCC CTTATTTGG TGGCAGAAGT 150
25 GGCCTCCACC CCTTCACCGT TAAAAATAC TCCGTGGAGA AAAGAAAGCT 200
TNAAGGAGTA G 211

(2) INFORMATION FOR SEQ ID :696:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :696:

40

GCCTGCACCG ACAATGCCCA GAACTCCAGA ACTTCACCTA TCACGTATCC 50

354

CCAACAACAC AGACGGCGAA AACAAAACAA ACTTAAACCT AG

92

(2) INFORMATION FOR SEQ ID :697:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :697:

15

GCCAGCACCG AGGCCTAGGG TAGAGCAGAC TGTGGCTTTA CCTCGGTGTC

50

CTACCAGCAA GGGGTCCTAT CTACCACCAT CCTCTATGAG ATCCTGCTAG

100

GGAAGGCCAC CCTGCATGCT GCGTTGGTCA GCACCCTTGC GCTGATGGCC

150

20

ATAGTCAAGA GAAAGGATTT CTGAAGGCAG CCCTAGAAGC GGAGTTAGGA

200

GCTTCTAACC CGTCATGGTT TAAATACACA CCCTTTTTTG GACAGCGCTT

250

25

CTGAAGAGCT GCTCTTACCT CTCTGCATCC CAATAGATAT CCCCCTATGC

300

GCATGCGTAC CTGT

314

(2) INFORMATION FOR SEQ ID :698:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :698:

40

GCCACCGCCG AGTTCACCCC TGCAGTGCAC GCCTCCCTGG ACAAGTTCCT

50

355

GGCTTCTGTG AGCACCGTGC TGACCTCCAA ACACCGTTAA GCTGGAGCCT 100
CGGTAGCCGT TCCTCCTGCC CACTGGACTC CCAACAGGCC CTCCTCCCCT 150
5 CCTTGCACCG GCCCTTCCTG GTCTTTGAAT AAAGTCTAAG CGGGCAGC 198

(2) INFORMATION FOR SEQ ID :699:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :699:

GCCAGCACCG ACAGCAACAA AAATGTTCCC ACAGAGATCA GGATGACTTG 50
20 CTGAAGCTCA GTGGAGGCTA AAAAGAGGAC ACAAAGTGA ACAGAATGAC 100
CTTCCTACGC ACAACACAAA CACCAGTTAA TGCTCCATCC ACGCTGCTTA 150
25 AAGAGCATTG CTGTCCTAGC AAAATGGGCA AGTCCCTCTA CCCCCACCC 200
TTAGCCGGCA TGCTTACATT AATAGCTAGA 230

(2) INFORMATION FOR SEQ ID :700:

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :700:

40

AGCAACAAAA ATGTTTCCAC GGAGATCAGG ATGACTTGCT GAAGCTCAGT 50

356

GGAGGCTCAA AAGAGGACAC AAAAGTGAAC AGAATGATCT TCCTACGCAC 100
AACACAAACA TCAGTTAATG CTCCATCCAC GCTGCTTAAA GAGCATTCCCT 150
5 GTCCTAGCAA AATGGGCAAG TCCCTCTACC CCCCACCCTC ACTTGGCATG 200
CTTACATTAA TAGCTAAAGT CAATCCTGTA ATGAAATAAA GCAAATGGCA 250
GCTGTCTAGT AGCCTCCACT ACCGCAAATA TC 282

10

(2) INFORMATION FOR SEQ ID :701:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :701:

GCCTGCGCCG AACAAACGCA CGGAATGAGC GAGTCCCTCT GGGAGCCCAA 50
25 CATGGATCCG AATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100
CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150
GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC 200
30 CTGTTCCCAG AGCCCACTTT TCCCCTATTT TGGAATAAAA ATAGCCTGTC 250
TTTCG 255

35

(2) INFORMATION FOR SEQ ID :702:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

357

(xi) SEQUENCE DESCRIPTION: SEQ ID :702:

5 GCCTGCGCCG AGCACAAGAC AATGATGAAC ATTCTAAAAA AAAAGAATGA 50
CGCACATTTT AATAAAGCAC AGCACAAACT GTTCTTTCC 89

(2) INFORMATION FOR SEQ ID :703:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :703:

20 GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGCCGC ACCCCCGCTA 50
GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GTCGGG 96

(2) INFORMATION FOR SEQ ID :704:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :704:

35 GCCTGCGCCG AACAAACATA CAGAACGCAA CGAGTCCCTC TGAAGGCCCA 50
ACACGGATCC GAATCACCTG GCCCGAAACC ACCTACCTAG CCATGATGAA 100
40 TGCTGAGGAC CCAGATGCAG TAC 123

(2) INFORMATION FOR SEQ ID :705:

358

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :705:

10 GCTTGATGCC TCGCCGAAC AACATACAG AATGCGGCGA GTCCCTCTGG 50
ACGCCCAACA CGGATCCGGA TCACCTATCT GAAACCATCT CCCAAGCCAT 100
15 GCTGAATGCT GCGGACCAGG ATGCAGTGCC AGGCATGGGA GCCATTGCCC 150
ACATCACCGA GAAGGACAAA ATCACCACCA GGACACTGAA GGCCCGAATG 200
GACTAACCCT GTTCCCAGAG CCCACTTTTT TTCTTTTCA GAAATAAAAC 250
20 AGCCTGTCTT TC 262

(2) INFORMATION FOR SEQ ID :706:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :706:

35 GCCAGCACCG ACCTAGCCTA AGCCGTCTAA AACCACCTGA GCCCCTGAGG 50
AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCGCAGAGG 100
CGTGTCTTAG CACTGCCCCC CTCCTAGCC CTTATTTGG CGGCGGAAGC 150
40 GGCCTCCACC CCTTCCCTGT TTGCAAACAC TCTGCGGAGA AAAGAGGACT 200

359

TCAGGGAGT

209

(2) INFORMATION FOR SEQ ID :707:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :707:

15 GCCAGCACCG AGATGACGAG CTTTCTGCTG CCACCCACAA GCAGAGGGAC 50
TCGGAGATCA CGCAGCAGAA GCAGAAAAG GCAAACAAGA AGAAGGAGGA 100
ACCCAAGCAG CTTTGCGGCT TCACGCCCAA CCCTCTCGCC CTTACCTGT 150
20 GAGCCTGGAG CCAGTCCCAC 170

(2) INFORMATION FOR SEQ ID :708:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :708:

35 GCCACCGTCG AGGATTCAGC AGCCTCCCCC TTGAGCCCCC TCACTTCCCG 50
ACGTTCCGTT TCCCCCTGCC CGCCTTTTTC CGCCACCACC GCCGCCGCCT 100
TCTGCAGGCC GTTCCACCG AGGAAAAGGA ATCGTATTGT ATACCCGCTA 150
40 CCCAGAACCT 160

360

(2) INFORMATION FOR SEQ ID :709:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :709:

GCCAGCACCG AGCAACCTGG GTCCAAATAA AACTAAACT GCAAATCCT 50

15

G

51

(2) INFORMATION FOR SEQ ID :710:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :710:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

30

CAGGATTCTC TTCT

64

(2) INFORMATION FOR SEQ ID :711:

35

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

361

(xi) SEQUENCE DESCRIPTION: SEQ ID :711:

CCAGCCAAAG ATTCCCAGGC TTTCTTGTCT CAGCAACTTT CCCATCTTCT 50
5 CTCTCTTGGA TGATGTTTGC CGTCAGCATT CACCAAATAA ACTTGCTCTC 100
TGGG 104

(2) INFORMATION FOR SEQ ID :712:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :712:

20

CTAGAAATAG ACCCACAATT TAGAGACAAT CTATACTAGA TTTATCTCCT 50
TTGTTTTTAG TTGAAGGC 68

25

(2) INFORMATION FOR SEQ ID :713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :713:

AGCGAATGTA AGGGGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT 50
GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT 100
40 GTGCTTGGGT CGCTGTCTAC TGCTCCT 127

362

(2) INFORMATION FOR SEQ ID :714:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :714:

CTTGGGAGAT AACAGTTTCC CCTCTCCCTC CCCCTGCAGA TTTCCAGCGC 50
15 CCGGACCAAG GCCAAGTAAG CCTCTACAAA CCTAGCATTT 90

(2) INFORMATION FOR SEQ ID :715:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :715:

CCAGCGCCGA GGTGTATAT TTGTAGGTGC AGGCACACGA CCAGGACACA 50
30 ACAAAAATCT GAAAACATC 69

(2) INFORMATION FOR SEQ ID :716:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

363

(xi) SEQUENCE DESCRIPTION: SEQ ID :716:

GCCGAGGAGA ACCCCCGCTC CCTGAGGAGG ACCTGTCCAA ACTCTTCAAA 50
5 CCACCACAGC CGCCTGCCAG GATGGACTCG CTGCTCATTG CAGGCCAGAT 100
AA 102

(2) INFORMATION FOR SEQ ID :717:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :717:

20

AGCGAATGTA ACCCGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT 50
GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT 100
25 GTGCTTGGGA TACGCTGTCT ACAG 124

(2) INFORMATION FOR SEQ ID :718:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :718:

40

GGAAAACCGT GTACTATTAG CCATGGTCAA CCCCACCGTG TTCTTCGACA 50
TTGCCGTCGA CGGGAGCCCT TGGCGCGCGT CTCCTTTGAG CTGTTTGCAG 100

364

ACAAGGTCCC AAAGACAGCA GAA

123

(2) INFORMATION FOR SEQ ID :719:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :719:

15 ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC 50

TTCT 54

(2) INFORMATION FOR SEQ ID :720:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :720:

30

GACCACAGGG CCTTCAATCC TTTTTTGTTT TCAACAGTCT TGCTGAATTA 50

AGCAGAAAGG GCCTTGAATC CTGGCCTGGA ATTTGGGCAG ATATAGCATT 100

35

AATAAACTG TGCACTC 117

(2) INFORMATION FOR SEQ ID :721:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

365

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :721:

GACCACCCCT TCCTTTTCTT CATCCAGCAC AGCAAGACCA ACGGGATTCT 50

CTTCT 55

10

(2) INFORMATION FOR SEQ ID :722:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :722:

GACTTCACGA ACTACACAGG TCTTACCATT GACCTAAGAT CAATCTGAAC 50

25 ATTCTTAGCC CAGTCAGGGA GCTCTGCTTC CTAGAAAGGC AT 92

(2) INFORMATION FOR SEQ ID :723:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :723:

TATTTCTAGG TGCAGGTATA TGATTGCCAT ATAATAAAAA TCTGAAAACA 50

40

TCCCC 55

366

(2) INFORMATION FOR SEQ ID :724:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :724:

GTGTACTATT AGCCATGGTC AACCCCACCG TGTTCTTCGA CATTGCCGTC 50
15 GACGGGCGAG CCCTTGGCGC GCGTCCTTTG AGCTGTTTGC AGACAAGGTC 100
CCAAAGACAG CAGAAAAATT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA 150
TTTGTTTATA AGGG 164

20

(2) INFORMATION FOR SEQ ID :725:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :725:

GTGAGAAGCT GCAGCGGTGA CCTGGAGGCT GCGATGTGGA GGTGGAGGAC 50
35 ACACCCTCAA CCGTTGCTCC TGTAGCTTCC GAGTCCTGGT GGTGTCGGCC 100
AAGTTCAGTA 110

40

(2) INFORMATION FOR SEQ ID :726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs

367

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :726:

CCGTGTACTA TTAGCCATGG TCAACCCAC CGTGTTCTTC GACATTGCCG	50
TCGACGGGAG CCCTTGGCGC GCGTCTCCTT TGAGCTGTTT GCAGACAAGG	100
TCCCAAAGAC AGCAGAAAAT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA	150
TTTGATTATA AGG	163

(2) INFORMATION FOR SEQ ID :727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :727:

GAGGGCGAGT TCGAGGAGGA GGCTGAGGAG GAGGTGGCCT AGAGCCTTCA	50
GTCAGTGGGG AAAGCAGGGA AGCAGTGTGA ACTCTTTATT CACTCCCAGC	100
CTGTT	105

(2) INFORMATION FOR SEQ ID :728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

368

(xi) SEQUENCE DESCRIPTION: SEQ ID :728:

5 GCCAGCGCCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG 50
ACCTAAGATC AATCTAAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCT 100
AGGAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTCGA GGCCGCCACT 150
10 GGAAGACGAA AAATAGAACT CCCTTAGAGT AGACAA... 186

(2) INFORMATION FOR SEQ ID :729:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID :729:

25 GCCAGCGCCG AGGTTGCATA TTCTAGGCGC AGGTATATGA TTGCCATATA 50
ATAAAAACCT GAAAACATCC CACCCGGGAA AAAAAAAAAA AAAAAAAAAA 100
AAAAACACCC CCCCCCACA AAAAATCAA ATTCCCCTCC CAAAAAACCC 150
30 CCTCAAAATC AAAAAAC 167

(2) INFORMATION FOR SEQ ID :730:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 40

(xi) SEQUENCE DESCRIPTION: SEQ ID :730:

369

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

CAGGATTCTC TTCT 64

5 (2) INFORMATION FOR SEQ ID :731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :731:

GCCAGCGCCG AGACCCTGGC GGCCTACCGG CCCCCCGTGC ACCCCCGCTA 50

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

20

(2) INFORMATION FOR SEQ ID :732:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :732:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

35 CAGGATTCTC TTCTGCAGCC GCCACCGCGT CGGA 84

(2) INFORMATION FOR SEQ ID :733:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double

370

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :733:

GCCAGCGCCG AGATCCTGGC GGCCTACCGG CCCTCAGTGC ACCCCCGCTA 50

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

10

(2) INFORMATION FOR SEQ ID :734:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :734:

GCCAGCGCCG AGATCCTGGC GGCCTACCAG CCCTCCGTGC ACCCCCGCTA 50

25 GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

(2) INFORMATION FOR SEQ ID :735:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :735:

GCCAGCGCCG AGATCCTGGC GGCCTACCAG CTCCTCAGTG CACCCCCACT 50

40

AGCACCCAC CCCGCATCTA TCGCCCAATA AAGGCATCTT TGCCGGG 97

371

(2) INFORMATION FOR SEQ ID :736:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :736:

GCCAGCGCCG ACCACAGGGC CTTGAATCCT TTTTGTTTT CAACAGTCTT 50
15 GCTGAATTAA GCAGAAAGGG CCTTGAATCC TGGCCTAGAA TTTGGGCAGA 100
TACAGCATT ACAAACCGC GCATCTC 127

(2) INFORMATION FOR SEQ ID :737:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :737:

30

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50
CAGGATTCTC TTCT 64

35

(2) INFORMATION FOR SEQ ID :738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :738:

5 GCCAGCGCCG ACAATGCCCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC 50
AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :739:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :739:

20 GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGTGCA CCCCCGCTAG 50
CGCCCCACCC CGCGTCTACC GCCCAATAAA GGCATCTTTG CCGGG 95

(2) INFORMATION FOR SEQ ID :740:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :740:

35

GCCACCCCGA AGACGTATCA AGGCCCTCGA ACAACCCCGA GAGCTGATGA 50
GATGAATGAG AAGATGCCGA ACTTTGCGCA CTCCATGCCC CTGCTGCAGA 100
40 CAGTAACCAA GAGCAAGGAC CAGGGCACCC ATGAGGATTA TGTCGAAGGA 150
CTTCGGGTGT TTGACAAGGA AGGAAATGGC ACCGTCATGG GTGCTGAAAT 200

373

CCGGCATGTT CTTGTCACAC TGGGTGAGAA GATGACAGAG GAAGA

245

(2) INFORMATION FOR SEQ ID :741:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :741:

15

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTCGTCTAT CACTCTCCCC

50

AACAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG

88

(2) INFORMATION FOR SEQ ID :742:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :742:

30

GCCGGAGCCA AAGCAAGCCA GAAGACTAAC AGTACTAACT ACAAATATTC

50

GCACCTCGAT CGCAGTACCC AGGTTCTCAC GTAGCTGAAG NAATGTATTA

100

35

CTCTGATAGT CTTCAATCGG ATAGACTAAA GCGTGTGCTG ACTGGAGATG

150

AGGTAAAGAA GATATGTATG CAACGTCCAG TCAAACGGA TGGCAAGGTT

200

CGAGTCATGT CATATACCTT GCTGGATTAA TGGATGTCAT TA

242

40

(2) INFORMATION FOR SEQ ID :743:

374

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :743:

10

GCCTGCGCCG ACCACCCCTT CCTTTTCTTG ATCTAGCACA GCAAGACCAA

50

CGGGATTCTC TTCT

64

15

(2) INFORMATION FOR SEQ ID :744:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :744:

GCCAGCGCCG AGGTTGTATA TTTCTAGGTG CAGGTATATG ATTGCCATAT

50

AATAAAAATT TGAAAACAT

69

30

(2) INFORMATION FOR SEQ ID :745:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :745:

375

GCCAGCTCCG AGGTTGTATA TTTCCAGGTG CAGATATATG ATTGCCATAT 50

AATAAAAATC TGAAAACATC CCAC 74

5 (2) INFORMATION FOR SEQ ID :746:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :746:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTGTCTAT CACTCTCCCC 50

AACAACCTAG ATGTGAAAAC AGGATAAACT TCACCCAG 88

20

(2) INFORMATION FOR SEQ ID :747:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :747:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTGTCTAT CACTCTCCCC 50

35 AACAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :748:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

376

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :748:

GCCAGCACCG ATGAATTCCC TTTGACCCAA GTCTGCAGCA GGTCCCTTTT 50
GCGCTTCCTT CCCCTCAGGC AGCCTCTTTC CCCCTGGGCC ACTCCCGGGG 100
10 GCGAGGGGGC TACCCCTTTC CCAGGCTTTT TATCCCGTG GGGCTCACCC 150
CAAAGCATTA AAAGCAGCTT TGCAATTC 178

15 (2) INFORMATION FOR SEQ ID :749:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :749:

GCCAGCACCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG 50
ACCTAAGATC AATCTGAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCT 100
30 AGAAAGGCAT CTTTCGCCAG TGGATTCGCC CCAAGGTTGA GGCCGCCATT 150
GGAAGACGAA AAATTGCACT CCCTTGGCGC AGACAAACAC CAGTTCCCAT 200
35 TGGCGCTGCT GCCTATAACA AACACTTTTT TTTT 235

(2) INFORMATION FOR SEQ ID :750:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

377

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :750:

GCCTACGCCG AAAACCCCTT CCTTTTTTTC ATCCAGAAAA GCAAGAGAAA 50

AAGGATTCTC TTCTGCGGCC GCCAACGCGT CGGAGAT 87

10

(2) INFORMATION FOR SEQ ID :751:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :751:

GCCTCCGCCG ATTCGTGACC AAGAAGGCTC TATGCATTCA GGCTTTCCAG 50

25 GAGACTCAAA AGCTGAAGAA GCAAAGAAGA GCCTTAAAGG CTGCAGCAGC 100

AGTCCNAAAA ACAAGCAGAG CAGAGGAACC CAGACAGCCC TGCCAAAGCC 150

ATGCCAAAGA CACTCAAAGA 170

30

(2) INFORMATION FOR SEQ ID :752:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :752:

378

GCCAGCACCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT 50

AATAAAAAAA TGAAAACACC CC 72

5 (2) INFORMATION FOR SEQ ID :753:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :753:

GCCAGCGCCG AGGACACCAA GAAGGTTTTG GACAGCGTGG GCATCGAGGC 50

GGACAACAAC CAGCTCAACA AGGCCATTAG TGAGCTGAAT GAAAAAACA 100

20 TTGAAGACGT TATTGNCCAG GA 122

(2) INFORMATION FOR SEQ ID :754:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :754:

35 GCCACCGCCG ACTGAACTG CACCGACCCC CCCTCGAGGA CCTGCTCTTA 50

GGTTCAGAAG CAAACCTCAC GTGCACACTG ACCGACCTAA GAGACGCCTC 100

AGGCGCCACC TTCACCTGGA CACCCTCAAG CGGGAAGAGC ACTGTTCAAG 150

40 GACCACCTAA GCATGACCTC TACGGCTGCT ACAGCGTGTC CAGTGCCCTG 200

379

CCGGGCTGCG CCGAGCCATG GAACCATGGG AAGACCTTCA CTT

243

(2) INFORMATION FOR SEQ ID :755:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :755:

15

GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT

50

AACAAAAACC TGAAAGCATC A

71

(2) INFORMATION FOR SEQ ID :756:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :756:

30

GCCACGCGCG AGTGACGCCA AAGCCCTTGG TTGACTCTAA CAGCCCCGTG

50

GGCGCGCGGG AGGCCGGGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT

100

35

TAGTGCTTTT TCAGTGGGGC GGGGCGGGAA GCAGGCGGGA CCAGGCAGCC

150

AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA

200

GACGTCGCCA ACCAGAACTG ACGCGCGACC TCCTGGGCGC TGA

243

40

(2) INFORMATION FOR SEQ ID :757:

380

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :757:

10

GCCTGCGCCG ACCACCCCTT CCTTTTTTTT ATCCAGCACA GCAAGACCAA

50

CAGGATTCTC TTCC

64

15

(2) INFORMATION FOR SEQ ID :758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :758:

GCCAGCACCA AGTGACGCCA AAGCCCCTAG TTGACTCTAA CAGCCCCGTG

50

GGCGCGCGGG AGGCCGAGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT

100

30

TAGCGCTTTT TCAATGGGGC AGGGCAGGAA GCAGGCGGGA CCAGGCAGCC

150

AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA

200

35

GACGTCGACA ACCAGAACTG ACGTGCGACC TCCCGGGCGC CGA

243

(2) INFORMATION FOR SEQ ID :759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

381

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :759:

GCCACACCAG ACTTTCGACC CCCCAACCCT CTGAGGAAGA TGGGGGCAAG 50
AAGATCACGC TCCCCGCCTG TTCCCCCGCC GCTTTTCTCC TCTCTTCTCT 100
10 CTTGCTCTC AGCTCCCCCT GTCCCCTCAG CTCCAGACGT AGGGGAGGGG 150
TTGCCACAGA CTCCCTGCTT GAAGCCTGCC CTTGCCTAAG ATGCTGGTAA 200
15 TGGCCATGGT ACCCCCTTCC GGGCATCTAC TCTGGTTTTT GCCTA 245

(2) INFORMATION FOR SEQ ID :760:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :760:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT 50
30 AACAAAAACC NTGAAAAC 68

(2) INFORMATION FOR SEQ ID :761:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

382

(xi) SEQUENCE DESCRIPTION: SEQ ID :761:

5 GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50
AATAAAAACT GAAAACACCC C 71

(2) INFORMATION FOR SEQ ID :762:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :762:

20 GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTGCTAT CACTCTCCCC 50
AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :763:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :763:

35 GCCTGCGCCG ACAAACAAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCCGA 50
GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC 100
CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG 150
40 CGCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG 200

383

CGGATAGTCA CACTCCCTGC CGA

223

(2) INFORMATION FOR SEQ ID :764:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :764:

15 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50
AATAAAAATC TGAAACACCC 70

(2) INFORMATION FOR SEQ ID :765:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :765:

30

GCCAGCGCCG ACCGCCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50
TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAAA CCAACCACC 100
35 TTTCTACGTA CCGTATAG 118

(2) INFORMATION FOR SEQ ID :766:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

384

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :766:

GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTGCCTAT CACTCTCCCC 50

AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

10

(2) INFORMATION FOR SEQ ID :767:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :767:

GCCACCGCCG ACTCCAGGCA CTCACTCAAA CTTGATCTTC AACTCTGCAT 50

25 ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTTCAAT T 91

(2) INFORMATION FOR SEQ ID :768:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :768:

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA 50

40

CATGGATCCG GATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100

385

CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150

GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC 200

5 CTGCTCCCAG AGCCCACTTT TTT 223

(2) INFORMATION FOR SEQ ID :769:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :769:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC 37

20

(2) INFORMATION FOR SEQ ID :770:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :770:

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC 37

35 (2) INFORMATION FOR SEQ ID :771:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

386

(xi) SEQUENCE DESCRIPTION: SEQ ID :771:

5 GCCACCGCCG ACTCCAGGCA CTCACTCAA CTCGATCTTC AACTCTGCAT 50
ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTTCAAT T 91

(2) INFORMATION FOR SEQ ID :772:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :772:

20 GCCTGCGCCG ANGCATTCCC TTGACCTGA GTCTGCAGCA GGTCCCTTTT 50
GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGGG 100
GTGAGGGGGT TACCCCTTCC CAGTGTTTTT TATTTCCGTG GGGCTCACCC 150
25 CAAAGTATTA AAAGCAACTT TGCAATT 177

(2) INFORMATION FOR SEQ ID :773:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :773:

40

AACATAAGAG GAGAAAGGAA GGGACATGAG GCATACCATT CCCCCCCCCA 50

387

GAATTAGAGG TAAAGGAATC CTAAAATAAA GAGCACAGCA GCAATCACAC 100
TCACAGGGTC CAGAGGCGTA TTCCTGGCCA TCTTCCTAGT ACTCGGTCCG 150
5 T 151

(2) INFORMATION FOR SEQ ID :774:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :774:

ATCTTAATGA ACATGGCATT TAAAATCCTG TAATTTCAA CAGTGAACCA 50
20 CAATGCCGTA TGATCTAAAG GCTGCTGAAC CACAGCGTGG ATACACTTAA 100
CTGAGCTCCT CGCTGGGTCA AAGCACTCAT CTCCGAGTCT AAAGCTACAC 150
25 ACTATGGAGC ACACAACTCT GCCTCGCGCT GACACCAGAC AAACACGGCG 200
GGAGCTGAGG CGGACAGCTA CAGGACCACG AGCATAGACC ACGGCACCTG 250
AGACCATCTC TACGCAAGGA CTTAAGGAAG CAAATATAAT ATTAAAATA 299

30

(2) INFORMATION FOR SEQ ID :775:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :775:

388

TGAAGGAAAT GACTACCTTG CACTACATGA AAAGGATATC GTTGCCATTG 50
TGGCGTAATT TTCGTGCCGA GTGAATGTGG CGCAAACAAC TATATATCNA 100
5 AACCGTATAT TTAAATGAA TTACTAGAGA GGAATGTAA TCATGGCAAA 150
AGAAATTAAG TTTAAGAAG ATGCTAGTGC TAAGC 185

(2) INFORMATION FOR SEQ ID :776:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :776:

20

ATCCAAGCCC ATACCCATCA ACAATGGGAC AGCGATTGGA TCACCAGCCA 50
TTTCACCACA CATGGCAACA AACTTACCTT CTTTAAGAGC GGCAGTAATC 100
25 ACATCGTCGA TCAAACGCAA AATCGATGGG TTATAAGGTC GATACAAATA 150
AGCAACCTTA TCATTACCAC GATCTGCAGC CATCGTATAA CCAATCAAAT 200
CGTCGGTACC AATCGAGAAG AAGTCCAATC CCTTAGCAAA CTCATCAGCC 250
30 AACAT 255

(2) INFORMATION FOR SEQ ID :777:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

389

(xi) SEQUENCE DESCRIPTION: SEQ ID :777:

	AGATTCTGCA GTGTAATATG ACCAAATCAA ATCCGTTGTA TGATCGAATA	50
5	AGGCCGTCAT AAAGTAAGTT GAAAATTTTCG TTCTTGGCTG AATCGTGTTA	100
	AACCGTTGTA CACAACGTAG TAAAATTCAT AACCCATCTG CATACCAATC	150
	GTCAGCCGTG ATGCATTTAC TCACTTTACG TCGATGAATG TCAAACATCG	200
10	CACCTTTTCA ATGTTTACTA AAAACATAGC ACGCAATAT	239

(2) INFORMATION FOR SEQ ID :778:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 252 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :778:

25	ACTGAACAAC GTAAGGTCTT GACTGACACT TACAAGTTGG ATGAATCTGA	50
	AATAAAGTTG GTATTGTTTG AAGCAGCCCA ACAATTTCTGA ACATGCTACA	100
	AGACCGTCGT TTGACTGACA AGGCCTTGAA GTACATGACT GACAACAACG	150
30	TCGATCTTCG CCTAGGCGCC ATGGTCACTG GTGTTGACGA AAATGGCGTG	200
	ATTTTAAAGG ATGACTCAAC TCGCCAAC TCGTTTCCTCA TTAGGACAAC	250
35	TA	252

(2) INFORMATION FOR SEQ ID :779:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 265 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

390

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :779:

	TCGGATTTAT ACGGCTGTTA GTGCTATCGG CGTCTGGTAT GTGTTATATA	50
	TCGCCTATCG TTTTGTGGCC AATGGGCGTT GGCTACGCGG GGCAATGATT	100
10	GCCATCGTTT TTGTTATCTT GACTTATTTT CTCATTTTAA ATATTATTTA	150
	ACTATTTTAC AAATAAAGTG GTCAAATGGG ATATTTTGCC AAAAATAGAG	200
15	AAAGTGTTAG GCGGCCACACA GCTGGAGGAA GAGAAAGCGG CTGTGCATGA	250
	AGTTATTGCA CCCGC	265

20 (2) INFORMATION FOR SEQ ID :780:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 249 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :780:

	CTCAGCTGGA CCAAATTAGT TGAATTACTC ACCATCAATA AACTATAAAT	50
	GGCGCCAATG ACCAACCCGC CAACGATTCC CGTTGTCAA GAACCTAATA	100
35	ACAAGTAACC AACCGCAGCC CCAACAAGCC CAACTAGGTT TAAAAAACC	150
	AAGCAAAAGG CCAACTGTCC GTCGTTTATT GGATTGTATC TGCTCATATA	200
40	ACATTAAAC TTAACCGTTG GCACTTCTTT CTCAGACCCG CCGATACTG	249

(2) INFORMATION FOR SEQ ID :781:

391

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :781:

10

GAGAGAACCC ACCATAGTAC TGTCTCCTGC AGACAAGACC AACGGCAAGG 50
CCGCCTGGGG TAAGGTCGGC GCGCACCTGG CGAGTATGGT GCGGAGGCCC 100
TGGAGAGGAT GTTCCTGTCC TTCCCCACCA CCANNNACTA CTTCCCGCAC 150
TTCGACCTGA GCCACGGCTC TGCCCAGGTT AAGGGCCA 188

(2) INFORMATION FOR SEQ ID :782:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :782:

30

AATATTTATT TCATTTGTTT ACTACCACTT CATTTTATTT GTTTGCTGCT 50
GCCGTTTAT TTATTTTAC TGAAAGTGAG AGGGAAC TTT TGTGGCCTCC 100
AACCTTTTTC TGTAGGCCGC CTTAAGCTTT CTAAATTTGG AACATCTAAC 150
AAGCTGAAGN GGAAAAGGGG GTTTCGCAAA AT 182

(2) INFORMATION FOR SEQ ID :783:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs

392

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :783:

10 CACAGCCAGA GCTTCGTCCT CAGTGACCAC AGGGCTGAGC CAGGCTCAAC 50
CGGCTTCTGG CTCTTGTTTT GCAGAAGAAG AACTAGAAGC AAGGNGCTTT 100
CCTCCGGGTC CCAGAGCTGT TAGTGATGGA GCCAGGCCTG GGATCCAGCT 150
15 TTCCTGAGTT CCTGACCCCT GCTATTTTAT TAGTCAGCTC TCAGCACTTA 200
CCAGAGGAAC AGGCAGCCTT TTGGCTACTG CCTTCAGAGA AAGAGAGATG 250
AGAGAATTCA AATGCGTGTT GGTGTTCCCTG TTAGTACAAG CAGCA 295

20

(2) INFORMATION FOR SEQ ID :784:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :784:

CAATAGCGAC TTCTGGTGTC AATTCGATAA TCGGCCAATG GATACTTCAC 50
35 GTGTGTTTCA TCGTCTGTAA TAACGGCGAA TGGTGTCCT TCAGAACCAG 100
TACCTGATGT TGTGGAATG GCAACCATTG GTGTCAAACG CACTGGTAGA 150
ACTTCACGAT ACGCTTACGG ATGTCCATGA ACTTTTGTTT TATTTCCATG 200
40 AACAAATTCCT TGATACCTTC TTCGTCTGAC AAAATACCTT CGTGACGTGT 250

393

TGAGTATTCG TACAAGAAGC GACCAATCTT ACCGGCATCA AGTGC

295

(2) INFORMATION FOR SEQ ID :785:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :785:

15 GTGTAAAGCG AGTAGCCCCC AAATCAGTCA TCTTGGCCTG AAGATGTAAA 50
CAAGGAGGTT TGCTTCCTGC AAGATGAGTA CTTCACTGAG TTTGGTTTTC 100
ATTTTTCCTA CACCGAAGCC ACCTCTGTCC ATCCAATGTT CATGTCTGTC 150
20 CGAGGCTGCG CAGGAGGTTA CGTCAAGATG TGGCCAATAA AGTCCAAAAA 200
GCGCTTTGAA TACTGTTCTG GGTTACGGT GGAGATCTCC GCGCAGCCAT 250
25 GTTTAACAGT TTTGCAGCA TGGGCAGCTT TCTTTTTTGC ATCATAATGA 300
GTA 303

(2) INFORMATION FOR SEQ ID :786:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :786:

40

TATGGCGCGG ATCCTAACGG CTGGAATGAA GATATGCCAA CGTACAGCCT

50

394

CTATGACCCA GCCATGGGAT CAGGCTCATT GCTTTTGACG ACTGCTTCAT 100
ACATGAAGAA TGATGGTGTT CGTGGGGCCA TTAAGTACTA AGCCAAGAAG 150
5 TTATCACGAC AACCTATAAC TTGGGCCGAA TTAAGTTGAT GATGCACGGG 200
GTGGAGTATA ACGATATCAA TATCCATAAT GCAGATACCT TGAGTTCAGA 250
CTGGC 255

10

(2) INFORMATION FOR SEQ ID :787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :787:

CATTGAAAAG TGCCTGAAAA ATGGTAAATT CTAAATGTG TGTGAGATTG 50
25 TCAGAATCAA CAAAAC TAGG TTGGTTAAAC ATATCTCTGG TACATCAAGG 100
GGCATGATAC AAACCACTCT AAAGACTGTT TATAAAGGAG AGAGCTGGCG 150
ACTTATTTTT ATTTTTTTTT TTTTGGACAG ACTCCCTTTG TCCCCAGGCC 200
30 GGAGTG 206

(2) INFORMATION FOR SEQ ID :788:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

395

(xi) SEQUENCE DESCRIPTION: SEQ ID :788:

ACAAATAGCG ACCTCCTGGA GAAAAATCGA AAACGGCCAA GTGGATACCT 50
5 CACGTGGTTC ACGTCTGAAC AACGGCGAAT GTGAGCTACC TCAGAACCAG 100
TACCCGAAGT TGCTGGAAGG CAACCACATT TGGTTCAAAC GAGGCGTGGA 150
AGAACCTCAC GACACGCTTA CGGAGTCCAT GAACGCTTGT TGCAATCCAG 200
10 GAACAATTCC GCGACACCCT TCGTCTGACA AAAACCTTC GTGACGCGTC 250
GAGTATCCGC 260

15 (2) INFORMATION FOR SEQ ID :789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :789:

AACCCACCAT GGTGCTGTCT CCTGCCGACA AGACCAACGT CAAGGCCGCC 50
TGGGGTAAGG TCGGCCTGCG CACTATGCGT GAGTATGATG CAGAGGCCCT 100
30 GGAGAGGATG TTCCTGTCCT TCCCCACCAC CAAGCCCTAC TTCCCGCACT 150
TCGACCTGAG CCACGGCTCT GCCGAGGTTA GGGGCCACGA CAAGAAGGTG 200
35 ATCGACGC 208

(2) INFORMATION FOR SEQ ID :790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double

396

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :790:

AAAAGAAGTA CGGTAAGGCA AATCCTGAAA TTAAGAGTTA CTATGTGCCT 50
GAAAATACAT TGTCTACTC ATTTAGTGTG ATGGCAATGG GCGCCGGCGC 100
10 ACTCTTGCTA TCGACCATCG TCGCGCTTTG GATGAACCGT CGTAAGTCAC 150
AATTAATGTA GACACAACGT CGATTCTCGT GACTTATGGG GATCGCAACT 200
15 TTCGCGCCAT TCTCGATCAA CACAGCCGGT TGGTCAGTGA CTGAATTAGG 250
TCGTTATCCA TGGGTTGTTT ATGGCTTGAT GCTAATAGC 289

20 (2) INFORMATION FOR SEQ ID :791:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :791:

TTTCCTGTGG AAGTAGTTAA ATTGATAAAT TCCAAAAATT TGGCAATTAA 50
TTGCTCATT TTAATGGTAG AGTTTCCATT AATGAAGTTG GAAAATACGG 100
35 TGAATCTTTC AATGAACTCA GTTAGACATT CGGAATGAGC TTCATACATT 150
GTCTTATTAT CTTTCTTCAA TTTATCCTCC AAATCTGGGA ATTCTGATAA 200
CCAAATTGAA GCACCTTATC TATGATCCGG GC 232

40

(2) INFORMATION FOR SEQ ID :792:

397

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :792:

10 TTTCAACAAA CAGAAACCAA TTTCCAACCA GAGGGCGATT TCTCCTTGTC 50
TGTAATATC GAACAACTA TTTTAAAGAA CTTGATTCTT GGCAACATTA 100
15 AGAGCGCTGT GAAAAATTCT CTAGAGAATG ACTTACTAAC GGAGGCCATG 150
GCGATCGCAT TAGATTCAAA TAACGAAAGA TCAAAGGAAA GTGTCAAGAA 200
TGCCTATTTT GCGAAGTATG GATCTAAATA AC 232

20

(2) INFORMATION FOR SEQ ID :793:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :793:

GGGAACATAT CTTACGGTA GTGANCCCAG TGACCAGATG TCTTATACAA 50
35 GTTCAAGTTA GACAAAACGG GTGTATACAC GTGTTGGTAA CCATTGGCCA 100
ATTCTTTGTC GGTGATGTAA CGTTCAACTT GACGGCGAAG CGATTGCCCC 150
ATTTGGTAAC CAACTGGCA AACCTGAACC CACTTCTTGA CTCGTAAAGA 200
40 ACAAGTCCAT GTCACGACCA ATCGTCCGGT GGTACGTTT TTTAGCTTCT 250

398

TCACGACGTG CAATTCTGCT TCAACGTCGG CTTGCTTCCA TT

292

(2) INFORMATION FOR SEQ ID :794:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :794:

15	CAGCAGGCAC AACACCATCG GTTGTGCTG AAAGTATTTT TAAGTCTTTG	50
	GCCAAGAAGT CAGTTTCAGC TAAGTTAGAC GGCACCTATG CGGGTATGCA	100
	TGATGTCATT CCTGCATCCG ATGATTTTTA ATTAATTACA ACAACTGATG	150
20	ATGAAGCGTC GAATTCGTCG CGTCATTCTG CCTCACACTC ACAGGCACAA	200
	GCCTTAAAGC ATTTGCCAAA GTTTGCTAAC ATGCACTTTG GCGCGGCAAC	250
25	CATTTATTGA AAATGGTTTC TACTATGATA CAAATAAC	288

(2) INFORMATION FOR SEQ ID :795:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :795:

40	GTGGCTATGT ATAAGCAGAT ATTATCTAGT AAATGTAAAG TGAACCCAAT	50
	CGATAGACCC AAAAAGTGTT TTAAGTGGAA AACACCTTAT GAGGTTTATT	100

399

TTGATGAAGT GTTGCAGTTG GTTTGATAAT TCAAGGCATT AAGGCAATAT 150
CTCAATCACC GCATTTTCCA CAACCGGCCA CAAAACAGCT CGTCTATTTT 200
5 GAGGTCAGTT ACGGCGTCCA GTCTTTGAGC AGATGATTG CCCCAGTGA 250
TCGTCGGC 258

(2) INFORMATION FOR SEQ ID :796:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :796:

20

TGCTTCAAAG CCTGGCTTAA CCCGCTTGCC CACCAACTTC AATTATACCT 50
GCCCTTTTGC CTAACATCTC ACCGACTCGG GCAACCATCG TATCAACACC 100
25 CGCGACTCGA TCCCCATCGT AAAATGATTG CGAACTAACA TTTAACACAC 150
AATAGATAAT ACCATCAGCA TAATGCAAGG TTTTACCATC CACGACCCAG 200
AGGCGATCAA TCGCGACTAA CCGTCGTTGT AATTCAGGAC TAGCGGTACG 250
30 CTCATGTAAC GCGACAATAT 270

(2) INFORMATION FOR SEQ ID :797:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

400

(xi) SEQUENCE DESCRIPTION: SEQ ID :797:

	AAATATCGCT GCGTGCAGCT GAGTTACTAG CTGTTGAAAC TTATCGTTAC	50
5	TTGTGTAGGT TGTCTGAAAC GGTCGCAGTC ACCGGTTAGC TTGATAAGTC	100
	AGGTTTTTCAG CAACTGTCAT CAAGCCATCA CGACCTATAT AAGCCACTGC	150
	AATCGCACTT TACATCATTAG ACCCTTAC TAGAAGTAAC TGGCCATCCT	200
10	GCCACCGCTT	210

(2) INFORMATION FOR SEQ ID :798:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 218 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :798:

25	ATCATAAGCG CTGGAAGTTG GGGCATTGTA CAGGGACAAC TTCGGCCTTT	50
	GTTAGCCCCA AGAGTCTACA CTCTGCCAAT GGTGCGCTCC ATAGGAAAAA	100
	CCACGGTCCA AGGCAAAAAC TACGAACCTC AGATAACCGC AAAGAGGATA	150
30	TCAACCAGAG GACGGAAATG TAAGCCTATT TTAGCCCAA TAACGAGACA	200
	AGTAGTTGAG CTAAATGC	218

35 (2) INFORMATION FOR SEQ ID :799:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 176 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

401

(xi) SEQUENCE DESCRIPTION: SEQ ID :799:

5 CCTATCAGAA TCCAATGAGA ACTACAATGG TGTGCCCAGA CGTAGAGCTG 50
AGAATAGCAT TACCAAATGG AACACGTGC TACAGTCAGG ATTAAAAAGA 100
ACAATACTAC AAACCAAGTA TATCAGGCTA TTATAGCAAA GGCTGCCATG 150
10 AACCAATACAA CACTGAATTA CTCGGC 176

(2) INFORMATION FOR SEQ ID :800:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :800:

25 GCAATTGCTT AATTGTCTTCT TCCTTCTTAG CATTTTGCTG AGAAGCCAAA 50
CGTTGCGCCA ATTCAGAAGA TTCACGCCAG AAGTCGTAGT TACCAACGAA 100
TGGTGTGATC TTACCAAAGT CAACATCCAA GATGTTGGTT GACACGGCGT 150
30 TTAGGAAGTG ACGGTCGTGG GATACCACAA TCACTAGGTT CGGGAAATCA 200
GCCAAGAAAT CTTCTAACCA GTTAATTGTC TGCACATCCA GACCGTTGGT 250
TCGA 254

35

(2) INFORMATION FOR SEQ ID :801:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :801:

5 ATCCAGGCCC ATACCCATCA ACCCTGAAAC AACGATTGAA TCACCAGCCA 50
TTTAACCACA CATTGCAACA AACTCACATT GGGTTCCGAG CGGCAGTAAT 100
AACACAGTCG ATCAAACGCA AAATAGATGG GCAATAAGGT CGATACAAAT 150
10 AGGCAACCTT ACAATTACCA CGATCTGTAG CTATCGTATA ACCAATGAAA 200
ATG 203

15 (2) INFORMATION FOR SEQ ID :802:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :802:

GACACAACCTG TGTTCACCTAG CAACCTCAAA CAGACACCAT GGTGCACCTG 50
ACTCCTGAGG AGAAGTCTGC CGTTACTGCC CTGTGGGCTA GGCGAACGTG 100
30 GATGAAGTCG ATGGCGAGGC CCTGGGCAGG CTGCTGGCGA TCTACCCTTG 150
GACCCAGAGG TTCTTTGAGT CCTTTGAGGA TCTGTCAACT TCC 193

35 (2) INFORMATION FOR SEQ ID :803:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

403

(xi) SEQUENCE DESCRIPTION: SEQ ID :803:

5 AACAAAAGTT GAAAATTTTA AATGGTCTTT TTATGGTTTG CGTGACCTAA 50
AAAGACAAAG TTTATCCTTG CCTTACTGTA TAGAAATGCG TCGTATCCAC 100
AATAGCGTAC AGATTTTTC CATTAAATCC GTGTTTATAT TAACAGATTC 150
10 GTTAAGTATC GTTTAAAAAG GGAGAGAGGG GATACCCTCT CTCTAGATAA 200
ATGGGTCATC ATTTAATCCC AAGAATGATG TCGATAAGTA CTTTCTAAA 250
CGATAACAAG AACCCAGTA GGTAGTATAG CAGTCTTTAA 290

15

(2) INFORMATION FOR SEQ ID :804:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :804:

AACTTGATGG TCGAGGCCAT CTCCTGGGCC GCCTGACGAT ACCGTGGCTA 50
30 AACAGGTACT GCTGGGCCGG AAGGTGGTGG TCGTACGCTG TGAAGGCATC 100
AACATTTCCG GCAATTTCTA CAGAAACAAG TTGAAGTACC TGACTTTCCT 150
CCGCAAGCGA ATGAACACCA ACCCTTCCCG AGGCCCTAC CACTTCCGGG 200
35 CCCCAGCCG CATATTCCGG CGGACCGTGC GAGGTATGCT GTCCACAAA 250
ACAGGG 256

40

(2) INFORMATION FOR SEQ ID :805:

(i) SEQUENCE CHARACTERISTICS:

404

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :805:

10	AGCAACCTCA AACAGACACC ATGGCGCACC TGACTCCTGA GGAGAAGTCT	50
	GCCGTTACTG CCCCTGTGGG ACCAGACGAA CGCGGATGAA GTCGGCGGCG	100
	AGGCCCTGGG CAGGCTGCTG ACCGATTTAC CCTTGGACCC AGAGATTCTT	150
15	TGAGTCCTTT GAGAATCTGT CCACTTCTGA TGCTGTTATG GGCAACCCTA	200
	AGACGAAGGC TCATGGCAAG AAAGTGTTCTG GTGCCTTTAG TGATGACCTG	250
20	GCTCACCTGG ACGACCTCAA GGGCACCTTT GCACAC	286

(2) INFORMATION FOR SEQ ID :806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :806:

35	TTCTTCATCA GATTTTACAT CTGCCTGATT AGAATCTTCT AACTGGCCT	50
	CAGAAGATGA TTGTTCAAAA CTTTTTCTAA GTTGCTGTAA AAAAATTCC	100
	ACGGACAAAG TAAAATGCAG TTCTTTATCG TTTAGCCAGT GTACAACAAA	150
40	AGGTCCAATC TTCTCTTCAT TTTAATTCAG ACTCAGAGAT GTAATAGATG	200
	GAAGAAGTGA AATGTCTGTG GCTGGGTTGA TGCTGGCTGC AATATGAAAG	250

405

TGGCAAAGTG CATTGCTATG CAGTGGAGTG TTACTGTGGA C

291

(2) INFORMATION FOR SEQ ID :807:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :807:

15

AGTTTAATCA GCTGCAATGA AAACAAACGT CTTTATTAG GCAGAATCCA

50

GATGCTCAAG GCCCTTCATA ATATCCCTTA ATTTAGTAGT CGAACTTAGG

100

GAACAAAGGA ACCTTTAACA GAAATAGAAC AACAAAGAAAG CGAACTTAGC

150

20

GATACTCGCG GGCCAGGGCA TTAGCCACAC CAACCACCAC TTTACGATAG

200

GCAACCTGCA CTGGAGGGGC GACTTCTCCG CCAAAGCGAC GGGCCAGCAC

250

25

ACAGACCAGC ACGTCGCCCA GGAGCC

276

(2) INFORMATION FOR SEQ ID :808:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :808:

GGCCTGCCAA CAGCATAGGG AAGAATCTCA TTGTTATACA TATTAAGAAT

50

40

CGATTCTAAA TAGACCTTTT TACCAGTCGC TGAAACTCTT AAATTAAGTA

100

406

ACATCGCTAG CTAATTTTCG TAATGGCCGA TTAATCTTGA AACGGCGGCG 150
AAGCTTGTTTTC TTCACACGTT TCCCTTCAGG TCCTTTGATG AATCATACTG 200
5 ACGTGATCGC TTATCGTA 218

(2) INFORMATION FOR SEQ ID :809:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :809:

AGCAACCCAG CGCTCAATGG TGCTAGTGAA CACAGTTGTG TCAGAAACAA 50
20 CCTCAAACAG ACACCATGGT GCACCTGACT CCTGAGGAGA AGTCTGCCGT 100
TACTGCCCTG TGGGCAAAGG CGAACGCGGA TGAAGTCGGC GGCGAGGCCC 150
25 TGGGCAGGCT GCTGGCGATC TACCCTCGGA CCCAGAGGTT CTTTGAGTCC 200
TTTGGGGATC TGTCCATTAC TGATGCCGTA TGGGCAACCC TAAGGCCAAG 250
ACTAATGGCA AGCAAGTGCT AGACGC 276

30

(2) INFORMATION FOR SEQ ID :810:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :810:

407

GACTCCACCT GAACGGGCCC CTTCTGAACC GCCTCTGTGG GAGCAGGCCC 50
CATCTGAGGA GGGTCCATCT GAGCAGATCC CTTCTCAACA GGTCCTTCT 100
5 GAGGAGGCTT ACTGCTTTTC TTACTCGATT TATTTTTCAG AGTTTCTTC 150
TTCGTACTTT TTTTAACGCA AGTATTTTGC TTTTATTCT CCTCCATT 199

(2) INFORMATION FOR SEQ ID :811:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :811:

20

AAACAGCACA ACCAATGACA GGATGCAAGA ACTGATAGGG CGCCGCAAAA 50
AAAAAGCGGG CCAAAGATGA AGTAAATAAA CGTAAGGGAG GTACCGAATC 100
25 TGGGGGGCTT GGCCTAGAGT AAGGGAGAGG AGCTTCAACT ATCTCAATAA 150
GGGCAAGAAA ACACAAACAA CTCCTTCATT CGTCCAAAAT GCTTCTGAAT 200
TGCACCACAA TTGACACACA CACACCTCAA AGCAGAATCC GCACTGACCT 250
30 AAGT 254

(2) INFORMATION FOR SEQ ID :812:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

408

(xi) SEQUENCE DESCRIPTION: SEQ ID :812:

TTTTTTTTTT AGCAATGAAA ATAAAAGTTT TTTATCAGGC AGACTCCAGA 50
5 CGCTCAAGGC CTTTCACAAC ACCCCCCAAT TTAGCAATAG ACTTCAGGGA 100
CCAAAGGACC CTTTAACAGA AATAGAACAA CAAGAAAACA AACTCAAAGA 150
CACTCGAGGG CCAGGGCCTC ACCACACCAA CCCCCACTTC CAAACAGGCA 200
10 ACCTGCACCG GAGGGGAGAC TTTTTCGCCA AAGCGACGGG CCAGCACACA 250
GACCAACACA TCGCCCAGGA ACCTGAAGTT TTCA 284

15 (2) INFORMATION FOR SEQ ID :813:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :813:

ATACAACAGC AGAACAGGT ATCCACGCAC AGTCCAGCAA CATTTCTTCT 50
GGTACAACGC AGCTTCAAAG TTCACATCAA ACGTTACTTT GTCATACCAA 100
30 GGCAAGGATG CTAACCTGAA GTCAATCACG CGAGTGATGT CATTCAACAAC 150
CGGTCACGGT GCCGATGTGA CAATCAAGAC TGAAGGCGAT GACGAAGAAG 200
35 CAGCACTGCC CGCCGATAAC CGCAGCGATG CAAAAAAAAAG AGCTAGACGA 250
CTGACGAAAC CTGAGAACCC CGAAGGACT 279

40 (2) INFORMATION FOR SEQ ID :814:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs

409

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :814:

10 AACGTGCTGG TCTGTGTGCT GGCCCATCAC TTTGGCAAAG AATTCACCCC 50
ACCAGTGCAG GCTGCCTATC AGAAAGTGGC GGCTGGCGTG GCAACAGTGA 100
CTGAGAAGAC CAAAGAGCAA GTGACAAACG CCGAAGGAGC AGTGGCGACG 150
15 GCGGTGACAG CAGTAGCCCA GAAGACAGCG GAGGGAGCAG GGGGCATCGC 200
AGCAGCCA 208

20

(2) INFORMATION FOR SEQ ID :815:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :815:

AAACCACGCT CAGTCAGGTT CCGGCAGCAG CTGCAGCATC TCATCTTCTG 50
CGACTCTCGG TGCCCTCTCC TTCCGATTTC CGGAAACATG GCCTCCGATG 100
35 TGGCTGTCTC TGACGACGTC ATCAAGGTGT TCAACGACAT GAAGGCGCAC 150
AAGTCTTCAA CGCCAGAGGA GGTGAAGAGG CGCAAGCAGA TA 192

40

(2) INFORMATION FOR SEQ ID :816:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

410

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :816:

GAGAGAACCC ACCATGGAGC TGTCTCCTGC CGACAAGACC AACGTCAAGG 50
10 CCGCCTGGGG TAAGGTAGGC GCGACAATG GCGAGTATGG TCGCAGAGGC 100
CCTGGAAAGG ATGCTCCTGT CCTTCCCCAC CATGTGAGAC CTACTCCACA 150
15 CACTTCGACC TGAGCCACGC CTCTGCCAGG TTAAGGGCCA CGGCAAGAAG 200
GTGCCCCGACG CGCTGACCAA CGCCGTGCGC ACGTGGACGA CATGCCCCAAC 250
GCGCTGTCCC CCTG 264

20

(2) INFORMATION FOR SEQ ID :817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :817:

ACCCTACACA CATCCGTTCA ACTGTCCCAT CACCCACTTA CACTCCAAAA 50
35 AAAACCACTC AACAGCAAA CAACCCATCC TGTTTTCATA ACGTTATCGT 100
AAC AAAG CCGACCATAA TCAACTTGAA TTTACTTCAC CACAAGGCAA 150
AGCGATTATT TAGATGAGGC ACTCGCACTA CTGCTTGAAG TGCTACTAGA 200
40 TG 202

411

(2) INFORMATION FOR SEQ ID :818:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :818:

AGTAGAAAAT AAGTTCAAAA TTTTAGAAAT ACTGGCTTTA TACTCGCCCA 50
15 TGTATTTACA TTCACAGAGA TCTTTATTTA TTTACAAGCG CTTTGAGTTA 100
CTGTATAGTT TTTTTTAACA AAAAAGCGTG GGGGGCTCCC TTTAGCATTC 150
CCCATAGGAT AGGTAATGAA CTTTTTGT 179

20

(2) INFORMATION FOR SEQ ID :819:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :819:

TGTGCTCTTA TGCTAGATTT ACGGACAGAT TTTCTTCTGC CCTGTAAACT 50
35 AATAGCATAG GAGCATTTTT TAATACGATT CGATACAAA AAGAATTTAA 100
GCAATCTCTC GCCGAGACGC ACAATCAAGA CCATTCATAT ACTGATCTAT 150
CCGCTGAATA CGAACCTTCA ATCGACTCAA TCCGTAAGTG GATCAAGTTG 200
40 TACGCGGGTC CACGAAGTGA CAGACGAAAA ATGAACGCAA GCTGATGTAA 250

412

ACGCATCACA

260

(2) INFORMATION FOR SEQ ID :820:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :820:

15 ACTCGGCACT TTCTTAGAAT AGACAATTTG CAAAATGTCC ATCCCAGGTT 50
CATCCTTGTA GCCTAATGTT TCCGTCACCG TTGCCACTAG TTAACGTGGG 100
TGAAC TTAT CTGGGAAACG GGTAACATCC GCGACCACAA CTAGACCATC 150
20 ATTTGACGTA ATGCCATCAG CACTCACCAA AACTTGGCCA ACCAACAGCC 200
TTTCCGTAAC TGAGTTTGAT TTCTCC 226

25 (2) INFORMATION FOR SEQ ID :821:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :821:

CACCTACATA TAGATGCACG AAGTACTTGC TCACTTTTTT TGGTTGTAAA 50
TTTTCAAAGC GTTGAAGGCA GCATTCTTAG CGGCACGGAT GTCCTTATCA 100
40 GTGAATGAAT CAGGCTTTTC CATGGCCAAC CAACCAACGA TTCGCATCGC 150

413

GTGATTTCTGA ATCATGTCAA GCAAAGCACC GGCTGTATCA TAGTAAC

197

(2) INFORMATION FOR SEQ ID :822:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :822:

15

GGACTGGGTG CAGTGGCTCA CACCTCACGT TACATTTTAT AGCTAGCAGG

50

GTAATGGGGA GTTATGGCAC TCAGGTCACA TTCTAGGGAA TGTTTATCGG

100

GCAATCTCAA TGGCACCGCA AGCTAAATGA CTTCCAGTGT TTCTCATCTT

150

20

TGCGCTTTCT TCATCGCAAC CTTTGCCCAA GACATCTGTT TTTTCTGGAT

200

CACCTTGCA CAGCCACTGA GGAATGATCT TCTGAAAGTG AATCTTCAGT

250

25

AGACACATCG CCACACCATC TANGTCAGCC ATCACATGCC CAGGTCTNGA

300

CATG

304

(2) INFORMATION FOR SEQ ID :823:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :823:

40

GGCCCAGCAG ANGGAGGAAC ACTACCGAGG CTCCAGCTTA ACGGTATTTG

50

414

GAGGTCAGCA CGGTGCTCAC AGAAGCCAGG AACTTGCCCA GGGAGGCGTG 100
CACCAANGGG GCGAACTCNC GGGGAGGCGG GCGACCAGGG TCACCAGCAG 150
5 GCAGTGCTTA GGAGCTGGGA GCCGACCGAG CCCACCGAAC TCGCGCG 197

(2) INFORMATION FOR SEQ ID :824:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :824:

20 AAAAACAATG TCATTTTGTA CAGACAAAAT TTAGCAGACT CAAGCTTCCA 50
CAGTTAGTGC GAGAGCCTGT GGATGGCATA GTTACATAAG AGTCTGTTGT 100
GGATTCAAAT GTCACCTCTT CCAGGCAGTC TTTCCTGACT TACCCTGGCA 150
25 GCTTTGTGTT CCCACATTAC TAGTAATGTT TTTTCCTTA ATAGCAATGA 200
TTTCACTGTA ATAATGTATT TATATGCCTC TCTCCCCCAG ACAGCAAGCG 250
30 TTTTCCCACA GGTCTCGACA CACAGAAGAT A 281

(2) INFORMATION FOR SEQ ID :825:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

(xi) SEQUENCE DESCRIPTION: SEQ ID :825:

415

TATTAAATTT ACTAGAATGT TACAGTTACA AATTTGGTAA TGTTCTTTCT 50
GAAAAACAGC CTAATTTTGC AGCCTGAAAC TTGACTGAAA ATCTCAATAC 100
5 TTTTATTCAT GATAGAAAAA TAATTCCTGG CTTCATCTCA CAATTAACTA 150
ATAATTATGT TAATATAAAA TATAACTGTG CCCTTTCTTT TCAGTGATGA 200
TCAAAGTGAT TCTCCCAGGC CAAAAATCA AATAAGAAGT TATATTTTAA 250
10 AAAGACATAA CAAGCCATTC TACCCAGTGG GCATCTTCAG TGTACTCCCT 300
CTACTAATTG GC 312

15 (2) INFORMATION FOR SEQ ID :826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :826:

ACACCAAACA CGGGGAGTGG GGAGTAGAGG CTCTGGAGGT CAGGATGGCA 50
GGGCAGGGAG GGAAGGAAG GAGTTGTTGG TCTCACAGTG TGCCTGCCAA 100
30 TCCCAAAGCC CTAGAGACCC CTTCCTGCA GCACCTGCCC CCGGGTCTCA 150
GGCAGCTTCA GGGCCAGAGA GCTGCCAAGG GCAAGCAAA 189

35 (2) INFORMATION FOR SEQ ID :827:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

416

(xi) SEQUENCE DESCRIPTION: SEQ ID :827:

5 CTCTTAAGGG CTTGAAAATT TCTGTGGGAG TAGGACAGAG TGTAGAACGT 50
ACAGTAAAAG GCAATAAAAC AGTGGGAATA ATTTTACCAG CTATGAGTAA 100
AGGAGTAATG GGTATTTACT GCCTGTCATT AATCCACACA TATATCCATT 150
10 TTAGAGATTA TTTTGTTGCC TGGAAATCTG TCTCATCACA GAGTGTTAAT 200
ATACACCGGC GGGATATTCA AGAGTGGCTA AG 232

(2) INFORMATION FOR SEQ ID :828:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :828:

25

GGACATTGGA ACACTATACT CTATTATTGC GGTCGTGCCT AGCAGTCTCG 50
CGCATGTCTC CTCAGCGCGC ACAGTCTCTC TCAGAGAGCT CTTCTCTCTT 100
30 TATATGCGCA GACCCGCAGA CTGGGAGACC CAGACCCAGG GCAAACCTCTC 150
TTCTTAGGTA TATCGCACCC ATCATATCTC ACACATCGTG TATGTCGTAT 200
CATCAGACCC CCATAGAGCA TATATGCTAA ATTAATGCTC TCTTTCATCA 250
35 GTAATTACCC CATATCATAA AATGCGGGCG GG 282

(2) INFORMATION FOR SEQ ID :829:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid

417

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :829:

	CACTACATCC GCAAGTACAA CCGCTTCGAG AAGCGCCACA AGAACATGTC	50
10	TGTACACCTG TCCCCCTGCT TCAGGGACGT CCAGATCGGT GACATCGTCA	100
	AGTGGGCGAG TGCCAACCTC TGAGCAAGAC AGTGCCTTC AACGTGCTCA	150
	AGGTCACCAA GGCTGCCGGC ACCAAGAAGC AGTTCCAGAA GTTCTGAGGC	200
15	TGGACATCGG CCCGCTCCCC ACAATGAAAT	230

(2) INFORMATION FOR SEQ ID :830:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :830:

30	TTCCGCAAAT AAAAGAATTC ACTAAGGTAC CAAAACAGAA AATATACAGA	50
	GATCAATGAC TTTCATATAC ATTAACAAAC AAAAGTTCAG AGATAAAATG	100
	GAAGAGAAAT GCTGTTTTTA ACAGTATAAT TAAGATAAAA TATGAAGGTA	150
35	TAACTTAAC AAGAAATGTT GCAAAACCAT TATGTGAAAA TTACAACACT	200
	CCTGAAGACG CAGACACACC TAACAA	226

40

(2) INFORMATION FOR SEQ ID :831:

(i) SEQUENCE CHARACTERISTICS:

418

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :831:

10	AGAAGTCCTT CCAAGAGTCT TGGGTATGCA ACAGCCATGG AGGCTGTGAC	50
	CTTTTTCCTT CTTTCTACA GCCTGCAGTT CATTAAAGGA TCACCGGAGA	100
	TGACTCGTGC TCTAGTTCTT AAAATCAAAC AAGGATCTGC CAAATCCAAG	150
15	ACCCTGAATT TGGCCCAAAT TTGTAGAAAC ATTGCTTTTT ACCACCCGGT	200
	GCACCAAAAA TACCTCCCAT TTCAAGGCAA CAACCGCTTT AATTGCT	247

20 (2) INFORMATION FOR SEQ ID :832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- 25 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :832:

	CACCAGGCAG GGGATCCCGG AGGGAAGCCC TCTGCCAGGG ACATGGTGAG	50
	GGCGTGGCCA TCACCCACGA AGGGAGCATA AATAACACTG GCAGGTGGGT	100
35	GGGCAGCAGG AG	112

(2) INFORMATION FOR SEQ ID :833:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid

419

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :833:

AGCCATTCCC ACTAGAGGCC AAACCGCCTG CCCACAGAGA TTGACAGCCA 50

10 ATGTTCATCT CATAACTCTC CTCCCAGCAG TGCACCAGTA AACTCAGATG 100

CCTGAGTGCT TGTGGCCACC ACACAACAGA TCGGCCTTC CTCTTCACTG 150

GCCCCTCGGC TGCTGCTGGG TCC 173

15

(2) INFORMATION FOR SEQ ID :834:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 base pairs

20 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :834:

TGGCCCATGG GAGCCCTTAT GAGCAAGTTT CCAGGTCCTT ATGACACAAT 50

30 TCCATCATTC TTCGGGTACA TCCTTACTCT CTGGCACAGT AGAGATGTTC 100

CAGACTTATC TTATATTTTC ACTTCCCCAT ACCTGGAATC AATCACTTCT 150

CCGAGGATGC TTGATTCCTT TTAGTGAAGA ACAGTCTTTG GAAACCAACC 200

35

GTCTAGGGAC ATCAAGTATG TTTGCCGCTA TTGGAGTGTC ATTGCTCCTG 250

AACCTTCTAA GTGGACACAG CTAGGAAATG TATGTGCT 288

40

(2) INFORMATION FOR SEQ ID :835:

(i) SEQUENCE CHARACTERISTICS:

420

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :835:

10	CTTTTCTATT TTCCTTAAGT GTCTGCCAGT CTGAGAAATA AAGGGACAGA	50
	GTACAAAAGA GAGAAATTTT AAAGCTGGGT GTCCGGGGGA GACATCACAT	100
	GTCGGCAGGT TCCGTGATGC CCCACAAGCC ACAAACCAG CAAGTTTTTA	150
15	TTAGTGATTT TAAAAGGGGA GGGAGTGAC GAATAGGGTG CGGGTCACAG	200
	AGATAACGTG CTCACAAGA TAATAGAATA TCACAAGGCA AATGGAGGCA	250
20	GAACGAGATC ACAGGACCAC AGAACTGGGA CCAAATAAAG ATTGCTAAGA	300
	ACGTCTAGGG	310

(2) INFORMATION FOR SEQ ID :836:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :836:

35

	TCAGTGGAGG AATTAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT	50
	GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA	100
40	GAGGTAATCA AAAACTTGAG CATGTATTTA AGGATCCATG ATTGAATTTA	150
	CATCTCCCAA AATGCCTAGC ATTCTTC	177

421

(2) INFORMATION FOR SEQ ID :837:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :837:

CCGTTGCACT TGGTGTGGC ATTCTGCAGG GCGGCACTCT CCCACTCTTC 50
15 CCGGCCTCGA GCCAACCTGA CGGCAGCCAG ATGGCAGTCG TAGTGCACAA 100
TGTGAAGTG GGACACGGTG CTGTAGCCCT GCTGT 135

(2) INFORMATION FOR SEQ ID :838:

20

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :838:

30

TCAGTGGAGG AATTAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT 50
GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA 100
35 GAGGTAATCA AAAACTCGAG CATGTATTTC AGGATCCATG ATTGAATTTA 150
CATCTCCCAA AACGCCTAGC ATTCTTCGCC ACATTACAGT AGCAACATCA 200
G 201

40

(2) INFORMATION FOR SEQ ID :839:

422

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :839:

10

TTCTTTGGAG TACATCCTTA CTTTCTGCAC AACAGATGAG AGATGTTCCA 50
GAACTTATAC TGTATCATAT ATTTTACCTC CCCCCCTATA CACCCTGAGA 100
TATACATATA CACTATCTCC GCTAGAGAGA TGTCTATGAC ATATCACTTT 150
CTGAGATGTA CACGAACGAG ATCTTTTGAG A 181

(2) INFORMATION FOR SEQ ID :840:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :840:

30

CATACAAATG ATTAGAAAGC AATACAGCCT TATTGCTGAT ATGGAGAAGG 50
TTTTAGTGAA CATTCAGAGG AGTTTGGAAG AAAGTCGCTG CACAATCTTC 100
ATGGATGACT TTGAGGGATT CAAGACTTCA GTGGAAGAAC TAACTGCATA 150
TGTGAGTAGA AATGGCAGGA GAACTAGAGT TCGAAGTAGG AGCTGGAAGA 200
TAATAACATG GGTTTAAAAA AC 222

40

(2) INFORMATION FOR SEQ ID :841:

423

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :841:

10 CGCTCAGCTG GTCTATCCTG CTCTTCCTCT TGTCCCTTGCT CTTGCTGCGG 50
CTCCTATCTA CCGGCTACCT GCTGCCCGCT TTGCTCCTGC TACCGGCTCC 100
15 GACTCTGGCG GAGGCTCTTC TCCTGGCTCC TGCCCCCTGCT CACAACTCCC 150
TCGCTTCTCC TCCTCCACTC TCCTCTCCCG ACTCCTGCTC CGACTTTTGC 200
TCTTACTTTT ATGCCTGCTA GGACTCCGGC TCTTGGGTTT CCCGAACATT 250
20 GTCATTGTTT TGGAATTCT CTTCAGCTT GGTCTTTTGC CGG 293

(2) INFORMATION FOR SEQ ID :842:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :842:

35 ATGAGGAGGT GAGGAAAAGG AGAAGTGCAG CTACCATCGA GTGATTCTTC 50
TGGGATAGGT GTCTCATTTA AATCTCATAA TCATCTTTTT TGGCAGGTCA 100
GTCAACTTCA GGCTCACAGA TGACAGACAG TTGGCCCAA GACACACAGG 150
40 AAATACATAA GTGACAACGG AATACAAGTC CATGAATTAA AAAACCATGC 200

424

TTTTCTCTCC TTGCCACACA GCTTTAGTTT GAAAAA

239

(2) INFORMATION FOR SEQ ID :843:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :843:

15 TTCCGAATTA TTGAATCTTC TTCTGTAACA TCACAATCTT CCTGGTTTTTC 50
AGAATAAACG CTCTTCTCGC TCGCCTCTCT CTGCACTCAC TCCCACCTCA 100
CTCACTCACT CTATAATAAA ATGTTTGCAC TCAATTTATA TAGTAGTGTT 150
20 TGTC 154

(2) INFORMATION FOR SEQ ID :844:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :844:

35 GTCTTTAATT GAGAAAGCTG GAGTGGAGAC CCGATCCCCT GGGAGCAGTG 50
CCAGGAGTTG GGTGGAGACT GAGTGGGGTT TGTGTGGGTG AGGGGGCATC 100
TACTCCTCTT GCAACAAGCC AGAAGTAGAA CAGCCTAAGG AAAAGTGACC 150
40 TGCCTTGGAG CCTTAGTCCC TCCCTTAGGG CCCCTCAGC CTACCCTATC 200

425

CAAGTCTGAG GCTATGGAAG TCTCCCTCCT AGTTCCTAG CAGGTTCCCC 250
ATCTTTTCCA GGCTGCCCCT AGCACTCCAC GTTTTCTGA AAAAATCTAG 300
5 ACAGGCCCTT TTTGGGTACC TAAAACCCAG CTGAGGTTGT GAGCTGTAAG 350
GTAAAGCAAG TTCTATCCAA TTAGAAGCTG TTGGGGGCGT AT 392

(2) INFORMATION FOR SEQ ID :845:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :845:

20

CAAAGAATAA ATAATTTTTC TATTCCTGAA AGTTAACTAA TTATTTATTA 50
GAAAGTCAGA AATATGTGGA AAGCAAAGGA ATATTGAGA AAGTGATATG 100
25 AAATTAATAA GTGGTAAAAA ATTAATAAAA TTAATATTAG AGTTTCCTTT 150
GAGCTAATCC TTTATTTATT TATTTTTTTC CTTGAGACAA TGTCTTGCCA 200

(2) INFORMATION FOR SEQ ID :846:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :846:

40

TTAAAAATAC TCTGGAAAGA GCACTTCCAT CGTTCATTTA CATCATATTA 50

426

	GAAATGGATT TCCGAGTCAG CACTGGCTTC CTCCAGAATA GCAGTCCTGG	100
	AGGAGCGAGA TCTCCCCAAG CCTCCAGGAT TGCAGTCTGT TTGTGCCTT	150
5	CACTCCCTAA TAGGTTTGCC TTATTTAAAG GACCCACCTT CAGAGCTGCC	200
	AAGGACTTTC TCAGAGCAGC TCCTTGGTCC CTCCGACAGC CTGGGATGGC	250
	ATTTATTCTG GGGCCTGGGT GTGGGGAGGT CCTCACCAGC CTAGGAGTAA	300
10	GAGGAGGTGG T	311

(2) INFORMATION FOR SEQ ID :847:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :847:

25	CAGATCAAGA CTGGTGCCCC TTGCCGATCT GAGCGCTTGG CCAAGTACAA	50
	CTCAGCTCCT CAGAATTGAA GAGGAGCTGG GCAGCAAGGC TAAGTTTGCC	100
	GGCAGGAACT TCAGAAACCC CTTGGCCGGG TAAGCTGTGG GCAGGCAAGC	150
30	CCTTCGGTCA CCTGTTGGCT ACACAGACCC CTCCCCTCGT GTCAGCTCAG	200
	GCAGCTCGAG GCCCCGACC AACACTTGCA GGGGTCCCTG CTAGTTAGCG	250
35	CCCCACCGCC GTGGAGTTCG TACCGCTTCC TTAGTCT	287

(2) INFORMATION FOR SEQ ID :848:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

427

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :848:

	GATTACAGGT GTGAGCCACC GTGCCTGGCC TATTAATATG CTCTTAAAC	50
	TCATCCATAC GTTTTCATAG CAAGAAAGCT TATTTCTCCC AACTACCGAA	100
10	TAATATTCTA TCGTATGGCC GCACCTCTGT TTATCCATTT ACCTATCGAG	150
	AGGCATCTTG ATTACTTCTA GCTTTGGATT ATTACAAATA AACTATACA	200
15	AACACGCAAA CAGAGTTTCT CGTGTGAATA TAAACCCGCA AACCGGCTGG	250
	AGGCATATNA CCA	263

20 (2) INFORMATION FOR SEQ ID :849:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 279 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :849:

	TTGTCAGTCA GAATAGGATG TAAAGACTA TTTCAAAGAG TTAAATTATT	50
	TGTTAATATC AGAGATCAGC CACAGACAAG AAGTTTATGG ATGAGTGCAG	100
35	CAGTGGTCCA TTGGACATGT TAAATACTCG TGGATATCCA CAATTCGAAT	150
	TGACATTAAA AACGAATGGA TACCCAACCTC TGAATTCCAT ATCGTTTTTT	200
	AATATCAAAA ACACAATTTT AACTACTGAT AAACCAGGCA ACCACCGCAA	250
40	GTTTATCGAA ATCCTGCCGC TACTAAACA	279

428

(2) INFORMATION FOR SEQ ID :850:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :850:

GCTGAAAGTT GAAGTGGAGA GCTTGAAACG AGAACTCCAG GACAAGAAAC 50
15 AGCATCTGGA TAAAACATGG GCTGATGTGG AGAATCTAAA CAGTCAGAAT 100
GAAGCTGAGC TCCGACGCCA GTTCGAGGAG CGACAGCAGG AGACGGAGCA 150
TGTTTATGAG CTCTCGACAG AAT 173
20

(2) INFORMATION FOR SEQ ID :851:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :851:

TCGAGAAAGT TTCAATGTGA TTAGATTAAA ATTAAAAGAA TCCATAAAAA 50
35 TGAACAAAG AAGAAGAGGA ATGAAATTAC TTTTACTTTA AACAGCATTG 100
TTATCACATA AAACACGTAT CTTACAAATT CATGGGATAG CCCATAAATG 150
GGACTACAGC AACAATGGTA GGAGAGTCCA TCCTTCTTCA AAAGCAACCC 200
40 AGCAGGAATT TTCTGTAAA AATATTTTTC CCGTAATACT 240

429

(2) INFORMATION FOR SEQ ID :852:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :852:

ACTGGACTGG TCAAGAACAA AGCTCATGGC AATAGTCTTT TGAATGTTA 50
15 AAGGAATTTT TCTAGTTGGC TTTCTGGAGG GCCAAAGAAC AACACATCT 100
GCTTATTATG AAAGTGTTTT GAGAAAGCCA AAGCTTTAGC AGAAAAACAC 150
CTGGGAAAGC TTCATTAGAG AGTCCTTCCC CATCACAACG CTTCTGCTTA 200
20 TTCCTCTTAT AAAACAAGGG CAATTTTGTG AGAGCTACTG ACGATTTTCC 250
CCTCGAAATT TACTATTTCT ACAGCTTATT AATCTCAAAT AGTAAGCATG 300
25 TCCTTGCCGT CACT 314

(2) INFORMATION FOR SEQ ID :853:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :853:

TCCTGAAATA CTCTCTACTG TCACTGCTTC AGTTTAATTT ATAGATAGCA 50
40 CCAGATATGA GTCCTTATTA GTTCTGATAA CTCTGAAATG GTTATTTGGT 100

430

ATTTCTTCAG TGACAAGCAA ACTATCCCCC CACATGCCTT TAATGGCCAG 150
TGTTTTCGAT TTGTATACCA ATAAGCAATC TAGGTAGAGG TAATCATATA 200
5 CTGATACGCT AACCTTTGAA ACATAATTC CAATCTAGTA AGCTAAAATC 250
GCGCCAATAC TGCTTAA 267

(2) INFORMATION FOR SEQ ID :854:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :854:

20

GCAGTGGATC TTTCTTTTTT TCCAAAGGAA ATTTTCATATA GAGTCCATTC 50
ATAGGAAACA GATAAAATGT GAACGGCTGC AACTGAGATG GGGGAGAGTG 100
25 GCTTGGAGCC CCCAGCCTCT TTGCTTTCTC TTATCCCTAT AGGATGGCCA 150
TTAGGTGAAG CAGTTTAGCT TGTGTTTCA GACCTG 186

(2) INFORMATION FOR SEQ ID :855:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :855:

40

ATTTTGAAAA GAAACCTACA AAAATTGTAT TTCCATATTT CATAGTCAGC 50

431

CAAAAATATT GGTCAACTCA TGCTCTCTGC AAGGTTCTGC AAAAATTGCG 100
GAGTGGTATA GACAAGGCAC CATTGCAATA TATAATACTT TTTGGGTATT 150
5 GGCCCAAAAA TT 162

(2) INFORMATION FOR SEQ ID :856:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :856:

TCTGTGGCCA CAGATGCATA TTACAAGCCC ATCCAGAGCC ATTATGAAGA 50
20 GAAAGTGGCA ATTTTATTCT CAGCCTGAGA AATCCACACC AATCTAGTCT 100
GGGTTTCCAA GGATCTGCCG TTTAAGTCAC TTAGCCTCTA TCCTTTCCGG 150
25 GAACAACCTG CCCCTAGAGA GGGTGAACGA GAATCGTCCC CAGTGCCTCC 200
AACATAACAA ACCCAATCGC CCTGTAACT TTAAATCTTC AACTCGAGAA 250
AAAGGCTCAT GACTACTTCT AACCATGCCC AAACCC 286

30

(2) INFORMATION FOR SEQ ID :857:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :857:

432

	AACTATATGG TATTATTTCA CGCTGTACCC AGTCCATTGC TTGAACTTAC	50
	GGGTACCTAA TGAAACGTGG AGGTCCGGAT GTATGAAAAT CTCCTCTTTT	100
5	CCCCTTTACT TACAGCCTCT GTAGGCAATA ATTATAGAGT AGTATAGATG	150
	ATTTTTCTTT TTTATAAATC TGCCTATCTC CAGGAGGATG GGGCGCGCAC	200
	TTTGTAGAAAT GCATATAAAT GCTCTACGCT CCTTTTTTCT GTTACTTAAT	250
10	CGGCGCCAAG GCCTTTACAT GAATACTCAG	280

(2) INFORMATION FOR SEQ ID :858:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 310 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :858:

25	CACTGGTTTT CATGACTGAT TTCTTTATTT TTAGTAGTTC TGACATGTTG	50
	GCCAGGCTGG TCTTGAAGTC CCAGCCAACC TCAAAGTGCT GGGATTACAG	100
	CTGTGAGCAC CAGCCCAACC TCGCCTCTTT AAAAAGAAAA AACACAAGTC	150
30	CACTCTGAAG TCAGCCTCTG TAACCTCCCC ACAAGAAAAC CGTTTTACAT	200
	CAGTCACTAA CCAAACAACC AACAGTGCTT CAACACAGAA AGTAAAGCAT	250
35	TATACAGGGC TTGAACTGTC TTTTAAGCAA GCCCCAAATC CTTTGAAAGG	300
	AGGCAGTAAC	310

(2) INFORMATION FOR SEQ ID :859:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs

433

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :859:

10	TCTGTGTGGA GGGGAGGGAC CCACTCTGGA CCCAGGTGTC ATCATCTCAG	50
	CCACAGCAGG GCCCTCTCAG GCTGGGAAAC TTCTGCCAGA GCTGGCGAGT	100
	CCTCTGCAGG TCAAGCCAGG GCTTGGACAC AACTACTTCA TCTATCGCGC	150
15	AGGAAGAG	158

(2) INFORMATION FOR SEQ ID :860:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 263 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :860:

30	TTTCTAATAA GAACATAAAA TAAAGGCTAA TTAAAAGAAG GTGACTGAGT	50
	CCAGGAAGGC ACTAATCAAA GATGATATAC AGCCAGGTAA AAAAGAACAA	100
	TTCACAGGCA CAAGACTATA TAACCATCGT TTTATTTTCA AACGTTATAC	150
35	AAAATATACT CTACCGAACT ATAATAGATC ATTAATAGTG GCACAATCTT	200
	TAGATTCGGA ATAACTTGAA AATAAATCCC AACCACGTAA CTTACTAAAG	250
40	GAATAATGAG CCA	263

(2) INFORMATION FOR SEQ ID :861:

434

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :861:

10 ATTTGTCTGA AAAATATATT TCTACACGAT CTGATAAAGT TCAGATAAGG 50
GGCATTCTAT TCCTAAGAAT GTCCTAAAAA TGGAAACTG ATAAAAGATT 100
15 ATGCTTAGAA TTATACAGGT AAAAGACCTA CAACAATTGT TCTCTTGTTT 150
TGATCCCATTA GGTCAATTGT TATTACTCTT CTTCAACAGA GTGATTTTCT 200
ATTATAAACT TTCTTAGGAG CCAATACAGA GTAGAAAGAA ATATTTTCAG 250
20 AAAG 254

(2) INFORMATION FOR SEQ ID :862:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :862:

35 GTTCCTCCTT TGTAATTAT GAAATATTTA TAGTTTAGAC TGAGTAATAT 50
GACATGAAAC AACAAACCTG CACATTTCTA ATTTATAACA AATCCGTTTC 100
CTTAATGGGT GGAAGGAAAT CTGAGGACAA TTCTAAGGAG TCTTGCTGTC 150
40 TTTCAGTGCG ATCTTCTAGT CATACTGAAG ACAATACCTC TCCAGATTGA 200

435

TCTTTCCCCT TCTTATACTC TTCCCGATCA ACGTCAATCA CACGCACCAC 250
TCCAGGTTTT AGACTTAGGT CATCCGTCTC TACCTGACTT CTGTTGCCCT 300
5 TCACCTACAC GTGGCTCGCT TTAGTTTGCT GAGCAGC 337

(2) INFORMATION FOR SEQ ID :863:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :863:

TGGTGGGTTC GAGCCCAACT TCAGCGCTCT TCGAGAAGTG CGAGGCGAAC 50
20 GGTGCGGGGG CGCCTCTCCT CTCCACCTTC CTGCGGGAGG CCCTGCAAGC 100
TCTCAGCGAC GACGCCACCA TCTTCTGACC AACTTCAGGC TACTACCCCA 150
25 ACTTACAATG CCACCGCGA 169

(2) INFORMATION FOR SEQ ID :864:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :864:

ATTAAGGTAA AGGAAGACTT TCCATTGTGA AGTAGAAAGA GTGTCCTGCT 50
40 ATTACTACCA TTCACATCTA GTTTGTGTGA ACTAGGGTTT TCTATCTTAA 100

436

CCCTGTAA AACAAGGAA AGAAATGGGC TGAATGGCGC ACCAGCTATG 150
CGGATAGCAT TATCTTCCTG TGTTCCAGAC TGAATGAAT TTATGAACAA 200
5 GGCAAGCACA CCATTATAGT AAATAAATC TTACCTAGTT TTCGTTTTTG 250
CATTTCTTAC TTCGCAGTAT TTCTCCCGCC AAGAGC 286

(2) INFORMATION FOR SEQ ID :865:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :865:

20

ATATAGTCCG CTAGGGATAG TGAAAAATTT GGGGCTTGGT TTAGATTGGA 50
GAGGTATATG GTGGGGTGTC TTATAAGGCT TAACTTTGGG AGGGCCCAGG 100
25 GCCTTGATTT CTGTCCCCCT TGCCTTGCCT GGCCTTTGAA TTGAAAGCTT 150
TGAATTAGGC CTTCATAGAT TTTAGTGTGC ATACAAATAA CACGATCTTT 200
TTATAAGGCA GATTATGATT CTGAAGGTTT AGTGTGGGAC CCAAGCTTTC 250
30 GCATTTCTGA TCTATAAGGT GA 272

(2) INFORMATION FOR SEQ ID :866:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

437

(xi) SEQUENCE DESCRIPTION: SEQ ID :866:

ATGCAGGAGA AGAAGGATGC CAAACTAAGT CAAAAAACG GAACGCAAAT 50
5 AAAAGGAATG AGCACGGTTA CAAAGTCACA GGATGAGTCC CTGGGATCTG 100
GGGCGGGAGA AGGGGTGAAT CAAGAATGAC TTGAGCTTGT TACTCCCTAG 150
CAGGCTGAGG GCGTGACACA GCAGCTCGAT GACAAAGAGG TCTATTATAG 200
10 TTTCTAACAC TACAACGCTA ACTTTTGGAA CGTATCTACT TCTAGCATGT 250
AGACAGATCT CTAATCGCCT GCCAGACGGT AAGCCGCAGG AATGCG 296

15 (2) INFORMATION FOR SEQ ID :867:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :867:

TATTTTATCT CAACATAATA AAAACGACTA TAAATCTTCC TAAGAGAATG 50
CTCTACTCCC AAGACTAATT TAAACTCGGG GATCGTCAGA GGGAGTGCCA 100
30 CTGTGACTTC TACGATGAAA GAACAAGGGA GAGAAGATCT TATCGACAAT 150
CATACAAAGC CATATATACG CTATTCCTCA ACTCACAGAG TTAATTAAAT 200
35 GTCACCAGGA TGGAAGAAAC CTTATAAGCC CCTATCTATC A 241

(2) INFORMATION FOR SEQ ID :868:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

438

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :868:

GGACGACTGC AAGCTGGAAC TACACACGCG CACTCGCTCA CACTACACAC 50
ACGCCACTCT CACACACTCT CACACACGCA CCCTCTCGCG CATGCTCTCT 100
CAAAGCCCAA TATAACCAAG GGGAAGGAAT 130

(2) INFORMATION FOR SEQ ID :869:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :869:

25 TTCAAATATT TATGTATGTT TGAACATTTT CATAATAAAA TGTTGAAAAA 50
CTAATGAGAA TGGCATAAAC AACATTTAAG CAATATATTT TGAAATTTAA 100
TTCAAATGGT CAAATTCCTG GAAAACACAA ACTCCCTTCA CTAACAGAAT 150
30 TGATAGAAAA TCTGAGTAGT TCACCATTGT TAAAGAAATG GAATGTGCCA 200
TTTAAAACCC TCCAATTGAA AATACTACAT ATAGTTACAA TAGGGAATTT 250
35 TCCCAAGCAC TTAACAATA AACAATGCCC TCTTTATACA AACCTTTCCC 300
AGTAATAGAA 310

(2) INFORMATION FOR SEQ ID :870:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs

439

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :870:

10	AAAGAGGCAA GTTCCTGGTG CAAAGGTGGC TCTGCAGCAT AATTTAGGCA	50
	TTGGAGGAGC TGTGTGTTGT AACACTCTAC AAGATGGGTT TTCCGGAAGC	100
	CGCCAGTTCT TTTAGAACTC ATCAAATTGA AGCTGTTCCA ACCAGCTCTG	150
15	CAAGTGATGG ATTTAAGGCA AATCTTGTTT TTAAGGAGAT TG	192

(2) INFORMATION FOR SEQ ID :871:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 250 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :871:

30	ACCATAGATG TGTTCCAGAG GCAAAAGAGA CACATTATCC TAGATGGCAG	50
	AACATGCTTT CAAAACATAT AAAACGTCAA AGTTCCAGAT CTTTCTACAT	100
	TTTAAATCCT GTCTGAGGAT GGCAGCTGAC TTTATGTAGC TGATAGACGA	150
35	CTAGAGTTTC ATCCAAATAC CTGACCACGA CTTCATGGAG ATTTGAATAA	200
	TCTATCCGAT GAGATTTATA TNTAAACAAC TCAACTCCTG TCGAAACAAA	250

(2) INFORMATION FOR SEQ ID :872:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 base pairs

440

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :872:

10	TCAGCTACGA ATTGCTTCCT TCTCACAGAA CTGTGACATT TATCCAGGGA	50
	AGGATTTTGT ACAACCACCT ACCAAGATTT GCGTGGGCTG CCCCAGAGAT	100
	ATACCCACCA ACAGCCCAGA GCTGGAGGAG AACTGACTC ACACCATCAC	150
15	AAAGCTTAAT GCAGAGAATA ACGCAACTTT CTATTTCAAG ATTGACAATG	200
	TGAAAAAGC AAGAGTACAG GTGGTGGCTG GCAAGAAATA TTTTATTGAC	250
	TTCGTGGCCA GGGAAACACA TGTTCCAAGG AAAGTAATGA AGAGTTGACC	300
20	GAAAGCTGTG AGA	313

(2) INFORMATION FOR SEQ ID :873:

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :873:

35	TAGATGCTGA TGGCAATGAC ACAATTGACT TCCCTGAATT CCTGACAATG	50
	ATGGTAAGAA AAATGAAAGA CACAGACAAT GAAGAAGAAA TTAGAGAAGC	100
	ATTCCGTGCG TTCGATAAGG ATGACAATGA CTATATTAAC GCTGCAGAAC	150
40	TTAACCATAC AATGACAAAC CCCGAAGAGA AGTTAATAAA TGAAGAAGTT	200

441

GATGAAATGA TCAAAAACGT AGATNATTGA TGACGATGGT AAGGTAACT 250

ATCCAGCGTT AGCACAAATG 270

5 (2) INFORMATION FOR SEQ ID :874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :874:

TTGGGCCATG TCCCCATTTT ATCTCCAAAG CCAGCCATGG TGTATTTCTC 50

TCTGCTTTTC TTCCATATTT CCAACCCAGA AATGACTCCT GTTCCCATAT 100

20 GTGATTATTA TATTGCGCTA ACCCAAGTGA TTAAGGATAA TCTCACTACT 150

TAATGACAGC TGATTATTTT CATCTGCAA CTTACTCAAG AATGCAATCC 200

25 AGACTAACAC GACAATAGGA CATCAAGCT 229

(2) INFORMATION FOR SEQ ID :875:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :875:

TTTGAAC TTT CAGCCGAATA CATCTTTTTC CAAAGGAGTG AATTCAGGCC 50

40 CTTGTATCAC TGGCAGCAGG ACGTGACCAT GGAGAAGCTG TTGTGTTTCT 100

442

TGGTCTTGAC CAGCCTCTCT CATGCTTTTG GCCAGACAGA CATGTCGAGG 150
AAGGCTTTTG TGTTCCTCAA AGAGTCGGAT ACTTCCTATG TATCCCTCAA 200
5 AGCACCCTTA ACGAAGCCTC TCAAAGCCTT CACTGTGTGC CTCCACTTCT 250
ACACGGAAC GTCTCGACC CGTGGGTAAC AGTATTTTCT GCGT 294

(2) INFORMATION FOR SEQ ID :876:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :876:

20

ATTTTGGTA ACATACATCA AGTGGCACTA ATTACACAGT AACTATAAGG 50
TAACTAACAT GAAACCACAG AACTGTAAC CTGCCACAGC TGCATGAACT 100
25 CGGGTTGTCC TGACCGAGCC CATCCCCAAA AAACCGCCCA CCCCAGAGCT 150
ACGCCAACAA AAACCGTTAT TAA 173

(2) INFORMATION FOR SEQ ID :877:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :877:

40

TAATCAAAG AGCTCTAAAT CTGTAATTC TTTCTCCTTT AAAAAAATGT 50

443

CTACTTTGTT TTGGTCCTAG GCATTAGGTA ATATAACTGA TAATATACTG 100

AAACATATAA CGGAAGATGC AGATGATAAA ACTAATTTTCG AAC 143

5 (2) INFORMATION FOR SEQ ID :878:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :878:

ACTGAATAAA CTGCTGATGT CCAGGTTTCAG TGGTTCCTGC TGTGGGACTT 50

GCGTTTTTCAC TAAGTGTGGC GTTAGATCCA TTAGTTCCCG AAGAGCCTCC 100

20 AGTGCTTCCT AATGCCCCCA AGCCAGGAGT AAACCCTGGA ATGAGGCCCA 150

GGGCTTCTAT TGCTAATGCC TGTAACCTT GCTGAATCTA TAACAGAGTC 200

25 TATACCGCTC TCG 213

(2) INFORMATION FOR SEQ ID :879:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :879:

AAAGAAGGAA AAGAAAGAAA TAACACTTAA CAGTCCATAA CAAAGTGTTA 50

40 ACGAGATAGA CACATGCTTA TTCAAACCAC AGATATGATC CAGTTAATTC 100

444

CCTTCTTAGA ATGTGCCCAT AGTGCCTTAT TGCCTCATAA TAATGATAAT 150
AATAAGAGCA ACAATAATAA CGGCACAAAC TCCAGTCGAT ACTGACAAAC 200
5 TACCAGAGTA ACCGTCATCC CCTTGAG 227

(2) INFORMATION FOR SEQ ID :880:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :880:

ATAGACAAAG TCCTTCCCAC TAGAACTTAC ATTCCAGTGG GAAGAATTAG 50
20 AAGCCTCAGG AATTCATTG CTTACTTTTA GTTGTTACTT CAAAAGTACT 100
TACATTTAAT CTGATTATTA ATTATTCGTC ATGAGCTTCA TTTTATTACA 150
25 TCCAGGGCAC AGTATGTGAA TTGTGTTTCG TTCCTTTAGG AAAAGGAAAA 200
ATAATCACTC TTACAAGGT A 221

(2) INFORMATION FOR SEQ ID :881:

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :881:

AATTGTGGTA TATTTCAATT AAAATCGATC AAAGACAGCA ACATACATTA 50

445

	ATCAGAGGAA AGCATCAATT AAATGCAGAA ACAAGATTTA AACAAAGATT	100
	CATATTAAAA CAATGATAAG TAATACTTAG AAAGTGCATC CTAGAGACAC	150
5	ATCATTCGCA TTTTGTAGAA AACAGAAACA TATTAGTGTG AAAAGATGTT	200
	AAAAAATGAA TATTAAACCG TCGAGCACAA CACACTACGC CGATAACAAT	250
	ACACCACAAG CGCCGTAATC CTGCCGACAC TGACACACTA CAGGCGTCGT	300
10	GGCGATCCGA	310

(2) INFORMATION FOR SEQ ID :882:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 177 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :882:

25	GTTACATCA GTGTGTAGGA TATGCTATCA CGTATGTGCA TGAGAAGAAT	50
	GGAGAAAATG GATCTATGCG GATGTCTGTA CACACACACA CACACACATA	100
	CACAACAAGC TTGCACATGT ATAGAGGATC CGAAATTCCA CCAATACTGA	150
30	CGAACTACAA ACGTAACAGC AGCAGGC	177

(2) INFORMATION FOR SEQ ID :883:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 152 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

446

(xi) SEQUENCE DESCRIPTION: SEQ ID :883:

CAATTCTATT TTCAGAGTTG ACTGTACTCT TTCCTCTGA AGATACACGT 50
5 ATAAACGCGA CCAACGAGGT CTCTCGTCCT AATAACAGGT TCAGGCATGA 100
ATCACCGTCT AACAGCTATT TAAACACCGC CTCTTCATAG AAGTAACGCC 150
GA 152

10

(2) INFORMATION FOR SEQ ID :884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :884:

CCATAATATA AGTATTTATC ATGTATTCTG TGTCTGGAAT ACAATTCAAT 50
25 GACCTATTTT AGAAAAATCT TTTCAAGTAC TGGCTGAAAG AGTGAGGGAT 100
ACATTAGGAG ACTGCAAATA AACTGGCAAT CACAAGAACT TTTTCGGATA 150
AAATGAAATT GTGCCGAAAT GTATACA 177

30

(2) INFORMATION FOR SEQ ID :885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :885:

447

CACAGCTGGA AGAGCGGAGA AATAGAATTG TCTTCAAACA ATATAAAAAT 50
TCATAAAGAA TAGAAAGACT ACTATGTGTG GGTCGGGAAA TTAAGTAGAA 100
5 TTTTTTTATA TCCACACTCT AGTATGAAAT GAGTACTTAT AGAGTAGAGT 150
GTAACATATT TAGACATAGT ATATATATAT ACAAGTGTA CAAATATATA 200
TATTAAATAT ATATATGTTT TATAGAAACA CAGAGCACAC A 241

10

(2) INFORMATION FOR SEQ ID :886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :886:

GTAGCAACCG GCGCTCAATA AAATTCAACC AGCAAACCTCG ACAAGTAACA 50
25 ACCATAAAAC CAGCCACACT AAGTCCAGCC ACCACTACTC AATAAAAATA 100
ACACGTATCT TCCACCGTAC AACCAATAGC AACTGCAGGC TACTGCAACG 150
CCATCCATAT ACCAAAAATG CTACTTACAA CACCACAACA 190

30

(2) INFORMATION FOR SEQ ID :887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :887:

448

CACGCTTTCT CTCACACAGC ACTAGCGCTC TCTCACTATC ACTCTTCTCA 50
CAGAGCTGCG CGCGAGTCTC ACTACTATCA AATATATCTG TCTCTTCTCA 100
5 CTCTATAGCT CTCTCACAGA TATATATCTA CATATAGCGC TCTCATTATA 150
CTATAATATT ATACTCTC 168

(2) INFORMATION FOR SEQ ID :888:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :888:

20

ACTGGGCGCG CTGGTGCTGA CATCTTCAAG AGCATCTGTC ACTGAATATT 50
GCCGATCTCG CAACCGGTTC CAGTTAGACA GAACATTGTG ATATTCAAAC 100
25 CACTTTCTCG TAATTTCCAA TGGAGTTGTA AAGTTTAATG AGACCTCGAT 150
AATCATATTC TAGTCCACTG TAGC 174

(2) INFORMATION FOR SEQ ID :889:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :889:

40

ACACCACACT TAAGGAATGG GAGTTATATT TCACTTCCCT GAGGCCAGAA 50

449

	TATATATATG TATGTATGTA TATGTGTGTG TGTGTCTATA TATATATATA	100
	TATAGACACA CACGCACATT ATACACACAT ATATATACAC ACACATATAT	150
5	ATATGTGTGT GTACAATATA TAAAAAATTA TATGGGAGAA AAGAAAGGCA	200
	AATCTCCCAT GGCAGAGAGG TATCCCAAAA AATTTTTTTG TGTGTAACAA	250
	AATATGTTGT GTGTATATAT ATATGCACAC ATATTTATGT GTATATATGT	300
10	ATATATATAT CTGTATATAC AGGTATA	327

(2) INFORMATION FOR SEQ ID :890:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 181 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :890:

25	TTTTTTTCTT GTCTCTCCCG CAGCGCGCGC CTCTCGCGGC GCTATCTCTC	50
	GCTCTCTCTC GCTCTCTCGA GCTCTCGAGA TATAGCCGAG ACACGAGAGC	100
	TCGCTCTCTC CCGCGCGAAG ATCTCACCCC CGCGCGCTCG CGCGATATAT	150
30	ATCTCCTCGC GCGCGCGCCG AGCGCGCCCC T	181

(2) INFORMATION FOR SEQ ID :891:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 207 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

450

(xi) SEQUENCE DESCRIPTION: SEQ ID :891:

	CTCTTTAATA GCAAGCGAAT GGTAATTACA TGGTCGGATG AGGTCCTCAC	50
5	TCTCAGGGGA GGGAGGAGGG AGCAGAGGTG GACAGGGTGC AGTATAGGAT	100
	TTACACTGTT TGAAGCATCT AACGAAGGGC AACAGTTTTT GGCAACCCAA	150
	TTCACAGTTT TGTAATTTAC AAGAGATTTC TTTGAAAGGA AATAGGAAGG	200
10	CAAAGAA	207

(2) INFORMATION FOR SEQ ID :892:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 198 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :892:

25	CTATCACTTC AGGGAAACAA ACAACTAACA GCCATCAATT CAGAGGGAAG	50
	TGATTTTACA GTAGAGTGAA CGAACTTGG GAAGGAAAAC ATCCAAGAGG	100
	CGTCTGTTTG ACGTGGGTAA CGTGGGGAAC GCATACTGTC TGGCAAGAAT	150
30	TCTACTAGGA CCACGGGAAA CAAAGCAGAT TAAAACACTC TCTACTCT	198

(2) INFORMATION FOR SEQ ID :893:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 96 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

451

(xi) SEQUENCE DESCRIPTION: SEQ ID :893:

CTTTAGAGAA TGCCTTGTGG AAAAAAAAAA AAATGGGCCC CAATACTTTT 50
5 TACTGCCCTT TATCAAAATT GTTGTGCATG GACCGGGCCA AATAAG 96

(2) INFORMATION FOR SEQ ID :894:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :894:

AATTGTATAC CAACATATAA ATTAAAAGTG TTATGCAATG AGAAACAATA 50
20 ATGGAAACAG CATAATACTA CATACTATCG CGCGGGGTTG TCGGCGTGGT 100
GGGCGTGCGT GTAGAGAGAG AGCAAGGGCG TGTGCGTGAG TGGGCGTAAA 150
25 GAGTGAGCGT GGGAGGGTGT GGTCCGTGGA GGTGTGTGGA GAGGTGAGTG 200
TGCAGAGGG GCGAGTGAT GTGTGATAAG TATAGCGCGC AAGAGGCGAG 250
GACAAAATAT ATATATATAT AGATATAATA GATATGAGAG AACACTAAAC 300
30 AATAACCACT ACTCACATAG AATAT 325

(2) INFORMATION FOR SEQ ID :895:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

452

(xi) SEQUENCE DESCRIPTION: SEQ ID :895:

5 ATAGTTGTAC ATTTTATGG GGTGCATGTG ATATTTTGAT ATGTGCATAC 50
AATGTGTAGC AATCAAATCA GGGTAATTGG GATATTCATC ACCTCAAACA 100
TTTATCATTT ATTTGTGTTG GAAACATTCA AACCTTTTCT TCTAGCTATT 150
TATCCATTGT TGGATACTTA TATCAATTCT ATATCTTAGC TGTGTGAAT 200
10 AGAGCTGCAA TAAATGTAGG AGTGCAGATA TCTCTTGAT ATACTGATTT 250
TCTTTCTTTT GTTATA 266

15 (2) INFORMATION FOR SEQ ID :896:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :896:

AAGAAGAGTC TTCTGCACAA ACAAACCAT AGTGTTGACA AATAGTCATG 50
GCCAATGGCA ATCTGATGGT CCAGCGGCCC TCGGATGACT CCTCTGCAAG 100
30 GAGCATCTTC AGGGTTCTAG GGAAGTCACA GGGGCAACAT ATTGGAAACT 150
AGCAGGCCCA GAAGACCGCC CCGCCCCCA TGCCCTGGCG CAGGGCC 197

35 (2) INFORMATION FOR SEQ ID :897:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

453

(xi) SEQUENCE DESCRIPTION: SEQ ID :897:

5 GATGGCTGGA GTAGATTAGG GCGTAGGTAG AAGTAGAGGT TAAGGAGGGT 50
GATGGTGGAC TATGATGGTG GGGATGATGA GCGCTATTGT TTTTGTGAA 100
TATTTTCTT CCGACTAACT CGCGCCCCAC TCTCTTGCGA GCACAAACAC 150
10 ACGCGCGCGT GTAAGCGGCG CGAGACACGC GCCCCTTCCC CT 192

(2) INFORMATION FOR SEQ ID :898:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :898:

25 TGGATGTTTT CATTGCAAAA TCATGAGAAA CTTAAGTGGG TTTTATGCAC 50
TTGATAGAGT TGGCAAATT GAACATGAA GTTAACTATT TAACTCAAGG 100
AATGGGCGGC AAACCCATCC CCTCGATTGA TAAAGAAGGG GAACATTTTT 150
30 ACATTAGAAC TGACACTGAA AACATAGCTC TTTTTCAGTC CACCCTGGTT 200
GCTCTAGTAG CCCACAGCCC AATC 224

(2) INFORMATION FOR SEQ ID :899:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

454

(xi) SEQUENCE DESCRIPTION: SEQ ID :899:

	GAGGTGATTT CTCAGAGTTT AGAGAATAGG ATGGGGAAAA TTATATTTAG	50
5	TGAGTTATAA CCAGAATTAC ATAAGACAGA TATGGAAATT TTATAAACAA	100
	AATGCAAAAT ATTCTAATGT TTCAATGTTC TACATGAACA TATAGGGAAG	150
	CATAGACAAT AGCCAAAAAT ATGTTCTGCA TTCATATACT AGTTCAAGTC	200
10	CGAGTCTGGC TACTTCTAG GTAGTGTGCT TTTTGTCAA TTATAAAGAT	250
	ATATTCCCTT TGTTTTTTGA AAACGAGTGA GATGCTTAA TAGAGTACAA	300
15	TTATCTCATT CAAAATGTAT GTTGTTCCT CTCGAGAATT GTGAAGGTTT	350
	TGAGATTGA TT	362

(2) INFORMATION FOR SEQ ID :900:

20

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| | (A) LENGTH: 310 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| 25 | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :900:

30

	GTATGTAGCC CAGTGGGTGT CTTCCACAG GGTAGGTACT CAGTTTGCTC	50
	TGGAGGGTGA CTCATACCTA AACAAGTGCA CATCTCCTTT CTCAGTAAAG	100
35	CCAAAGCAGG TTTCTACATT TGGAACAAAA GAGATCCTGA CCAGAGAGCT	150
	ATCACTGGTG GTCCACTTGG GCCCTCCTTG ATGGGTGTGT TCACTTAGAA	200
	AACCAAATTA CAGATCTGAA GGCTGCTGGG TAGGGACAGG ATTAGAACAA	250
40	AGGGAATGAG ATTGAATGTT ATTTAAGGGA TATTTCTGTC AAGTTTTGGT	300

455

TTCTCGATGA

310

(2) INFORMATION FOR SEQ ID :901:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :901:

15 TTCCCCCATG AGACCGTTAG TCTCTCTTTG CCTGGCTGAC TACCTGCATA 50
CAGTAGGCAC TCACTGCTGG AGTGAGGCAC TGA CTCTCC AAAGATTGCA 100
GGGGGCGGAG GAGGGAACCA CGAAGGCCTG GGAGGGGGCA TCTTTGGCCC 150
20 CCACTAACCA TCTCCCTATT TCTGCATCCT GGTGA 185

(2) INFORMATION FOR SEQ ID :902:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :902:

35 ACAAGCTGCA AGATCCTTCA CTTGAGGCTT TCAGCCTTAT TCTCCTCCTG 50
TCAAACA ACT AA ACTACTCC GATGTTTGAT GAAAATTAAA CTGCTACTCA 100
GGATACTGCA ATTACAAGGA GAGGGAATGA TCAGCCCAGG GAGGCTATTA 150
40 CGTGTGACCT TTGAGATGGA CCTGATCGCC CCTTTTACTT TTTAGACTAC 200

456

AAGTGCAGGG AGGTGGAGCT TATTTGCATT TGAATCCTG TAAAGAGTAA 250
GAATATGGAA AGGATGAAGC CTCATTCATT CGGGCATATT AAAAAGAAAT 300
5 TGCCTTCAGA AACACTTTGC CTTTAAATAT GTGTAGCTAC AGTAAGTACC 350
AATGGGCTAA CTAATTGAAG CTAACATTTT A 381

(2) INFORMATION FOR SEQ ID :903:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :903:

20

CATCAAGGGT TTTTCCTGCT GCAATTCTTG TCAAAACTG ACATATGTAT 50
ATCGTTCTCA ACTGGCAAGC TGTTAGACTG GATAGTCCAT GAATAATAGC 100
25 CTCTGCGCTG TTGCGGGTCC TGCGGAAGTC CTCGGAGCGG CCGTCGCGGA 150
AAGCTCGGCA AAGAGAGAGG CAGAGGAAAT CGAGCATCCA GCCGGCAGCC 200
ACTTTTTTTT TATCGGCACC AGGCCGCGTC CTCCTCCTCC 240

30

(2) INFORMATION FOR SEQ ID :904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :904:

457

CCCTGGGCAG GCTGCTGGTG GTCTACCCTC GGACCCAGAG GTTCTTTGAG 50
TCCTTTTGGG GATCTGTCCA CTCCTGATGC TGTTATGGGC AACCTAAGG 100
5 TGAAGGCCTC ATGGCAAGAA AGTGCTCGGT GGCCTTTAGT GATGGCCTGG 150
CTCACCTGGA CAACCTCGAA GGGCACCTTT GCCACACTGA GTGAGCTGCA 200
CTGTGACAAG CTGCACGTGG ATCCTGAGAA CTCAGGCTC CTGGGCAACG 250
10 TGCTGGTCTG TGTGCTGGCC CATCACTTTG 280

(2) INFORMATION FOR SEQ ID :905:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :905:

25 GTTCTAGTGG TAACTGCTGC TTCTGGAAAA TATTTAGAGA AACCAACGGT 50
AAAAAAAAAA ATAATAATTA ATACCGTTGG TTTCTACATA CACTCTCAAT 100
ATTTGCACGA GTAAAGCGTA GCAAGTTTAA CACAACTTAT GTAAACTTGG 150
30 AAAATTTTCC GAAATTTTAT TGACTTTTCT CGGTCTCTCC TATCTTTATA 200
TACACATCTC TCATGCACAC ACGCG 225

35 (2) INFORMATION FOR SEQ ID :906:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

458

(xi) SEQUENCE DESCRIPTION: SEQ ID :906:

5 GGTGCTGACA TCTTCAAGAG CATCTGTCAC TGAATATTGC CGATCTCGCA 50
ACCGGTTCCA GTTAGACAGA ACATTGTGAT ATTCAAACAC TTTCTCGTAA 100
TTTCCAATGG AGTTGTAAAG TTTAATGAGA CCTCGATAAT CATATTCTAG 150
10 TCCACTGTAG C 161

(2) INFORMATION FOR SEQ ID :907:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :907:

AGAGATATAT GCAATCTGGT AGTCCATTAA ATGAGAGTTA CACTTAAAAT 50
25 ATTTTAGTTC TTTTAAAGAA AAAGTCTCCA TGTGCTATTT GGGAAAACCT 100
TCATTGCCTA AAGACCCACT TGCATAATTA AGGCAGATGA TGATGATCTT 150
30 TATATATGCG CACACACACA CACACACGAC ACGACGACAC ACACACACAC 200
TCTA 204

(2) INFORMATION FOR SEQ ID :908:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

459

(xi) SEQUENCE DESCRIPTION: SEQ ID :908:

	AGTTTCTGCA TTTGGTCTGT GTGACTCTAT GGAGCCCAGG ACTTACAGAA	50
5	AAAGGTGTAA CTGGCTCTTA GGACTTTAAG CCACATTATG GTAGTAGACC	100
	TGCCGTTTTA TTTGACATGG TGAAATAAAC TACCACTCCT TTGTGGTACC	150
	ATATGGGCAG GACAGAGCTC TTCAACCCTG GCTAACAAGC CTGAAGAAGA	200
10	CCCTGTGAGG CCGCAGCAGC CATGGGAACT TCCCAAAGGA CAGAAATCCA	250
	CATTGGAACG TAGCATCCAG ATAGGTGACA GAAATTCCTT CCACCATATC	300
15	CAAATGTGTG TGTTTT	316

(2) INFORMATION FOR SEQ ID :909:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 307 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :909:

	CTAGTAACAT AGAAAATAAA CTTCACTGGG AATCTCTGCT TCCCGCGTGA	50
30	GGTGTTTAAT TCTTGGCATT TTTGTATTTT AAAGATGTAG CAACTTGTTT	100
	CAAGTTAGAG GAGATGGCAG GGTCAAAATT TTAGAACTG GATCCCACCA	150
35	CCACTGTGTT ACTTCCTAAA CCTGCATACA AATGTTCTGC CAACATGTAA	200
	TGTGCCAATA GAATTATACG GTGTGAACTG CATATCTCAG TATCTCCACG	250
	GGAAAAAAT GTGGTTGGGG CATGGAGGGG GGAAAGGGAA ACTTTTTTAA	300
40	GCTATTT	307

460

(2) INFORMATION FOR SEQ ID :910:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :910:

TTTTTTTTTT TTTCCAGGCA CCTAACGATT TGTTTTGCTC AATCAAACGC 50
15 AGACAGGCGT CTCCGAAGTA CCACCACTGG GATATCCTCG GACCAGCGCT 100
TAAACCGAAT CCCCACAATC TCAAACCTCA CCAGGCCAAA GGGAACACAG 150
TGACACAACA ACAGGGTTCC AA 172

20

(2) INFORMATION FOR SEQ ID :911:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :911:

GCATAGAGAG ATATATACAC AGAGAGGACA TACATATATA TATATAGAGA 50
35 CACAGAGACA GACATATAGA GATATATATA TACACAGCAT AGAGATACAG 100
AGAGATAGAG AGAGATACAC ATACACACAT TCATCAACGA GAGAGAAGAG 150
AGGAAAGAGA GAGAGAGCGA GCACAGACAG AGATAGAGCA CACAGAGAGA 200
40 TCGCGCAGAT CTATACAGAG GGATATTCAC CACATTGTAT ATGGAAAGCG 250

461

CATCT

255

(2) INFORMATION FOR SEQ ID :912:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :912:

15 CAAGCGAATG GTAATTACAT GGTCCGATGA GGTCCCTCACT CTCAGGGGAG 50
GGAGGAGGGA GCAGAGGTGG ACAGGGCGCA GTATAGGATT TACACTGTTT 100
GAAGCATCTA ACGAAGGGCA ACAGTTTTTG GCAACCCAAT TCACAGTTTT 150
20 GCAATTTACA AGAGATTCTT TTGAAAGAAA ATAGGAAGGC AAAGAA 196

(2) INFORMATION FOR SEQ ID :913:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :913:

35 ACTATCACTT AAGGGAAACA AACAACTAAC AGCCATCAAT CCAGAGGAAA 50
GCGATTTTAC AGTAGAGTGA ACGAACTNG AGAAGGAAAA CATCCAAGAG 100
GCATCTGTTT GACGCGAGCA ACGCAAGGAA CACATACCGT CTGGCAAGAA 150
40 TCCCACTAGG GCCACGAGAA ACAAAGCAAA TTAAACATT ATCCACTACA 200

462

CGA

203

(2) INFORMATION FOR SEQ ID :914:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :914:

15	CTGCCGAGCC ACCATGCTTG CCTGAAGCTT CGGCCGCGCC ACCCGGGCAA	50
	GGGTCCTCTT TTCCTGGCAG CTGCTGTGGG TGGGGCCCAG ACACCAGCCT	100
	AGCCTGGCTC TGCCCCGCAG AACGGTCTGT GTGCTGTTTG AAAATAAATC	150
20	TTAGTGTTCA AAACAAAATG AAACAAAAAA AAAATGATAA AAAAATCGGA	200
	TTCCCGGTTA ACACTGTGAC TTCAATTGAA ACACCTTTTT GTAGTATCTG	250
25	GAGGTGGACA TT	262

(2) INFORMATION FOR SEQ ID :915:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :915:

40	TGGGTTCTAA TGATGTGCTT GAAGAGGAAG ATTTTGATCG CACCACTGAT	50
	ACACGGAGTC TGTATTTTGC ATCCTAGAAT GATTAACCAG AAACAAAGAA	100

463

AGGAAAAAGG TAAATCAAT AATAAGATCA GCAGCTCTGG GACACAGAAT 150
AAAGAATGAA ATAATTGAA AAAAAAGGCA GGGCAGGCAA A 191

5 (2) INFORMATION FOR SEQ ID :916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :916:

AGACTTGGGG GTTCCTGGTG TGTGAGGGGT CCTGGGATAG CTAGGGGTTT 50
TCCAGGAGTT GTCCTTTGTT GTTTGTCGTG AAGAATTATA CTTTGTGTGT 100
20 GTGTGGGTTG TCCCATGTGT ATGCGTGTAG TGTGACAGTA TATGACCCCC 150
AGTGTGTGCA TATGTTTGTG TGGTTGTCTC TGAGTGATAT CCACCTCTCT 200
25 CTCCCCCTCT GTCTCTCTGC AGAGATATGT GTGGCGTCAC TGTACTCTTG 250
TG 252

(2) INFORMATION FOR SEQ ID :917:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :917:

TAGACAGAGT GACAGTGAGA GAAAAAGAGA GGAAGGAAAA GGGAAAAGGA 50

464

GTAGGGAAGG ATGAGGGAGA TAGGAAAGCA CCTAC GAG GCAGAGAGTT 100
TCCTGAAGGT CATGCGATCC TTTACCCTCA GAAACTTTCA GGCTGAAATC 150
5 ACCATCTCCG TTATCCCAAC AAACGCACTC TCCTACCTCT ACAAGCACTT 200
CAAGTAAAGC AGAAATCACA CCAATACTGA CGNGCTTCAA GCGCAAC 247

(2) INFORMATION FOR SEQ ID :918:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :918:

20

ATTTGGATTG AATTGCCTGT TGCACCTTTA CATTAAGTGT TGCTTAAATA 50
AACAAAAATA GAGCATAAAT TCAATATTCT ACTGTCTAAA CATTTTAAAG 100
25 CAATGGTTAT GCCATCATAA ACAAGTAAAA TGCACCTAAT TCGAGTCTTT 150
TGACACCTCT TGTTTTAAGT TTCCTGTATG ATAAAGTTCT T 191

(2) INFORMATION FOR SEQ ID :919:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :919:

40

CAAGAGTGAG ACTCCATCTC AACCAAAAAA AAAAAGAAAG AAAAAAAGAA 50

465

ACAACCTCCT CATTTTCAGA AGCGAACACA CCCCCGCCCC AAGATAGACG 100
ACAGAGACCG GACTAAGATT TAACCCAGGA ACTTTTCGCT TGGGCACCTT 150
5 CGAACAAACAC ACAACCCGCA AAACCATACA CGCTCCCTTG CCCGAGGCCC 200
AACCC 205

(2) INFORMATION FOR SEQ ID :920:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :920:

20

GACAAAATTG GGACTCTAAG TATTGCGCTT TTTTTCCTC TCCAACGACT 50
CGTTCCCTTT CAACAAATAG CACTTCAGTC CACTGTGTAC AGAAGTAATA 100
25 CATCTCCTAT CGTTAGTTGA ATAAATTCAC ACACCGCGTT TAAGAGATGA 150
AACCACGACT TCGTCAAGCC ACATTGATT GCCATAAGAT TCCAAAGAAT 200
TCTATCCTCT TAAAGCGAAC CACATGTAAC CCGAAGGTCC CCACCTATCA 250
30 AGGTTAGAAC TGATATTCAA ATTATAGACT CATTCCACTA AGCAAGTAAG 300
CTCTAAGCTA CAGGTTGATC ATA 323

35

(2) INFORMATION FOR SEQ ID :921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

466

(xi) SEQUENCE DESCRIPTION: SEQ ID :921:

5 AACATTGACG ACGCTAAGGA TGCCATGATG CCATGAATGG GAAGTCTGCA 50
GATGGACGGC AGATCCGAGT AGACCAGGCA GGCAAGTCGT CAGACAACCG 100
ATCCCGTGGG TACCGTGGCG ACTCTGCTGG GGGTCGGGGC TTCTTCCGTG 150
10 GGGACCGAGG CCACGGCCGT GGACTCTCTA GAGGCGGCGG GGATCAAAAC 200
TATAGAAACA ACAAGTTAGA GTACAGACGT 230

(2) INFORMATION FOR SEQ ID :922:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :922:

25

TATTTTTCCT GATGTTCTCC CTCCTCCAG TCCCCGACCT CCCACAGGCC 50
CCAGTGTGTG TTGTTCCCGT TCCTCGTGTC CGTGAGTTCT CATTGTTTCT 100
30 TGCCCATTTCT GAGGGAAAAC ATGCCAGTGC TTTCGCGTTC TTCCTCGCTC 150
TCACCCACCT CTCAGCTTAT CGCGTCGCGC GCGCAGTATA TTCGTCTCTC 200
TCTCCAGTCT CTCTCGCGAC ACACATCTCT CTTTGTAA 239

35

(2) INFORMATION FOR SEQ ID :923:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

467

(xi) SEQUENCE DESCRIPTION: SEQ ID :923:

5 GTCAGTTCAG TTGTGAACAA AGCCCTTTGT GTACGTTTTT AAATTTTAGT 50
TCACACGATA ACAATGCTTT GCAAGTAGGT GTAATTATTT TACTCCCATT 100
TTATGGATGA GAAAACAACA GAGAGGTTGA TTGGCCCCAC CTTCAAATCC 150
10 TGAAACCCGT CCACTCAATA AATTTTGT 178

(2) INFORMATION FOR SEQ ID :924:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :924:

25 CAGCTGGTCC CCCACTAAAA GAAGGGGCAG ACCACCACTA GCCAAAAGAG 50
ATAGCAAGAC TAACATCTGG AAGAAGCGAG AGGAACGCCC ACTGATTCCC 100
AAAAAAAAC TCCAATGGGG ATTGTGTGTC TGCTGTCTCG TGCTGTTTAT 150
30 TCTTGCTTCT TGTTGTAAAT TGCAGTACGA ACTTAAGAAA ATGAGACTGA 200
GCAATCTCAT GGTCTTGGA CATGTCTCAA GCAGAGTAAA TGGTAATTCA 250
35 GTAATCAGAG AGAAAGATAC CAAGGAATGC TTTTCTGGC CTATTCATT 300
ATTTTGGGG GATGAATTTA CAGTA 325

(2) INFORMATION FOR SEQ ID :925:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs

468

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :925:

10	ATGGCTATGA CCTGGGACAT GGAAACAGTG ACCTCCGCGT TCTGGTCCCG	50
	AGATCCTCGC ATCAGCGTCA TCGTGTGCAC CGGCTTGGGG GGCTGGAGTT	100
	CCGGTTTTCT TTGTTTTTTC TCTTTATTCG TCCTTTCTCA AAGATGGGAT	150
15	ACTGATCAGA ATCGTTCTGT ATATGCTTGG GACTGGATGG AAAGACTTTG	200
	AAGCAGCTGT GGGGGGCGGG AGGACACCGA CAACCAAACA GACGTGTTGG	250
	TTCCAGTCCT G	261

20

(2) INFORMATION FOR SEQ ID :926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :926:

	GTCAGCCTGG GCAATCACAA CGACAACAAA AGGTACAGTC TCAAGAGTCC	50
35	AACTGGGTTC AAATCCTGGC TCTGTACAT ACTAGCTGTG TGACCTTGGC	100
	CAAGTTTCTT AACCTCTCTG TGTGTATAGT CCTTATCTGA AAATGGGGAT	150
	AACCAACCAA GAGAGCTGAG AGA	173

40

(2) INFORMATION FOR SEQ ID :927:

469

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :927:

10

AACACTCAGA CCGGACGGGA CGAGGGATTC CCCTGCCTTC GCTTCCCTCC 50
CTCGCTTGCT TTGTAGTTTT CCCGCACCAG CCCGCTGCCC TGCGCCATCC 100
TAGGGCCTCG AAGCCCGGGG AATCTGTCCC ATCCTGTAAC GGGCCGCCCC 150
CTTNGATTTT TCTGCCCGTG CCACCGGAGG TTGCTGCGAC GCGCACCGAC 200
TCAGATCATT ACTACTGAAC TCG 223

20

(2) INFORMATION FOR SEQ ID :928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :928:

GTTATAATTA TTTACATGCT GCAACACGTC ACAACATAAA TTTACCAAAT 50
ATTTTCATGGT GGGATGCTGT AGGTTTCAGA TAATAGTTTT AAGATAAAAA 100
CCACAGATTA AGTGAAGACA CCCACAACCTT TAATGACTCT ACGACTCTCG 150
GTTGCTAAAT GCTAGAAGTC AAAAGGCAGT GTTTTTTCAG TCCTACCTGT 200
CATAACTTGC AT 212

40

470

(2) INFORMATION FOR SEQ ID :929:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :929:

TTAACATAAT ATTTTGAATA TATAGGGCTC ATAAGATATA TTATTAAATT 50
15 ATAAACAAAA TAATCAGGAA CTTAGTGTGG TGCCTAGTTT GATATATGAT 100
TACTTTTTGA AATGCACTAA ATTCCACAAA TAATGAAAGT ATTCTTTGTG 150
TATAATGTTA TGTTTGGTTA TTATGTATGG TCTTCGTATC CAAAGGTATG 200
20 ACATAACTTG AGTTTGTGTTG CTTGGTATTT ATT 233

(2) INFORMATION FOR SEQ ID :930:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :930:

35 AGTCTGTAAC GATACACCCA TAGATGTGAA TTATGTATAT TCGAGAAGGA 50
GATCAGATGG CATCCAGAAG ATAGTTTAGA TTTGAGCACA TTCATGGTTC 100
AGATGCAAAA TCAGATCATC AAATAGATCC AGCAATTCAC AATCATCATA 150
40 GCCATATCGC GTCACGTCCG CCGCACAAAG ATCCGCACCA ATTATCTATC 200

471

TCCCACCCCC CCCAGGCATT CAGCACCCGC AAAAG

235

(2) INFORMATION FOR SEQ ID :931:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :931:

15

CTATCTAGAA TTACTTATTT CACTTGAAAT GTATGGTTTC AGGAAAATTT

50

TCAATTTAAC TTGAAGGGAT TATCTCTTAT TTTGCTTGGA ATAATGGCAT

100

CTCAGAAACA TGGGTTTACC TGTGATTTTT TTGTTTGGGT GAATGCTTAA

150

20

AAACAAAAAA AAAATTTACA TATGCATTTT ATGGATACAC ACACACACAC

200

ACACACACAC ACAAAAAACA C

221

25

(2) INFORMATION FOR SEQ ID :932:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :932:

TGCTCTATTG CTATCTCCTG ATATAGGTTA TATATATATT ATGTCTTGAG

50

CGTCATGTCT TGTGCTACTA CACCGTGTTA ATCCCAGCTA CTCAGGAGGC

100

40

TGGAGGATCG CTTGAGCCCA GGAGTTCTGG GCTGTAGTGC GCTATGCCGA

150

472

TCGGGTGTCC GCACTAAGTT CGGCATCAAT ATGGTGACCT CCCGGGAGCG 200
GGGGACCACC AGGTCTGCCT AAGGAGGGGG TGAACCGGCC CAGGTCGGAA 250
5 ACGGAGCAGG TCAAAACTCC CGTGCTGATC ATGTAGTGGG ATCGCAGCCT 300
GTGAATTAGC CACTGCACTC CAGCCCTGAG CAA 333

(2) INFORMATION FOR SEQ ID :933:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :933:

20

AGATTTATGG CTGCTTTCAC TTGGCTCCAT GTTCTGCTGA TAATTAAACA 50
GTTTGTGTGT CCTGTCTTTC CTCAAAGGAA CTTGTCAACC TTTGGAATTT 100
25 TGTTTCATCTC AGAGGGACGT CTTAAGTACT CAGCTTTCTG AATGTTTAAG 150
AAAAAAATAA TACTTTTCAG AATTACCTAC CTCTTTCTCA TTTTTCAGCCT 200
GGGATCAATT ATTCCCTTTC AACTTTTTTT ACATCCTAAG TAGAAATAAA 250
30 ACTCTTTATT CTATTTTTTT TCAGTTATTG G 281

(2) INFORMATION FOR SEQ ID :934:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

473

(xi) SEQUENCE DESCRIPTION: SEQ ID :934:

AATCTTGAT TATGTTAATA TTAAATCTA ATAATAAGAT ACTGTAGAAG 50
5 TATTTTACAT TTTTGGGGTA TAGGCACAAA TATATACATT TAAATATTAG 100
TAATAGAATT GAACAATTAA CTATAAAATA TTATATCATA ATAACTGTT 150
GTTTTATCCC AAGGGTAGAG GGACTCTAAG TAAACTGTA ACAGAATCAA 200
10 AAGGTTACTG ATAGTTAGAA TGGGTTGAGA ACTATTTTAA CTTGGGAACT 250
TTAAATAAGT AAATCT 266

15 (2) INFORMATION FOR SEQ ID :935:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :935:

GGAAAACAAA TGTAAGGAGG GAATTCAAAT ACCTAGTTAA TCTATTAAGT 50
ACTAATAACT CATTAAATAA ATTAATAATA TTAAATGATC TGTGTGTTCC 100
30 ATGCAAATAA CAGAATGATT TCCACTGAAT AGTCATGATG GTTTAAAATA 150
TTACTCTAAC ACCAATAACA ACACGTAA 178

35 (2) INFORMATION FOR SEQ ID :936:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

474

(xi) SEQUENCE DESCRIPTION: SEQ ID :936:

5 ACTCAGCTCC GTGCGACCCA CATGGCCCCA GGCGGGGGGA CACCAGAGGC 50
TCCTCCATGA GCAGCAGGAG TGAGCGGAGG AATGTGCCCC ACAGCAACTT 100
TCCCAGCCAA TGCCACGATG GAGATGACAA CCCAGATCT GGGGANACAG 150
10 AAACCACTCA GAACGGCACA GGGTAACTGG CCCCAAACGC TGAAAGTTAG 200
ACTTCACCCG AATTACATTT ACCA 224

(2) INFORMATION FOR SEQ ID :937:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :937:

25

ATTTTTTTTC CCAAGAATCC CCAACTCAAT AAAACCGTGA AACAATTGCT 50
GGGGATGGGT AGAGAAAACC CATTTATAGT ACTTTTCTGC CTTCTTGTGG 100
30 TTTTCGGCTT TCGGATCAGG GACTGAAGAT AGAAGGAAAA AAAAAAAAAA 150
AAAACAAACA CAAAAACATT TCAAAAGAGA AAGGAAAAAA CTTTTTCCAA 200
CCAAAACCTCC TAAAAAACCC AAAACAGAA CAACCAATTA AACCCGACCC 250
35 GACACAATA CCAATGACTG 270

(2) INFORMATION FOR SEQ ID :938:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 bas pairs
(B) TYPE: nucleic acid

475

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :938:

	AGCCTTCTCC CTATTCGATA AAGATGGCGA TGGCACCATC ACAACAAAGG	50
10	AACTTGGAAC TGTCATGAGG TCACTGGGTC AGAACCCAAC AGAAGCTGAA	100
	TTGCAGGATA TGATCAATGA AGTGAATGCT GACGACAATG GCACCATTGA	150
	CTTCCACAAA TCTTCAACTA TGATGCCTAG AAAAAAGAAA GATACAGATA	200
15	CTAGAACTAA AGTCA	215

(2) INFORMATION FOR SEQ ID :939:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :939:

30	TGTCGTCCTT AATATTTCTN AGCCTTTTGT CATAGAGGTG GTCGGTTGGA	50
	CCTCAAAGCC TCCATCTAAT TTTTTTTGTC TATGTTTCTA TATCTCTCTC	100
	TTTTACGCTT CTTTCCCGGA CCGTCCCCTC CCTCTACAAT TATATTTACT	150
35	ACCTTCATGA TTGCTTTTTA TTATTTCTTT CACTCATCAT TATTGTTCAT	200
	TTTTTAATTA ACAATTTTTT TCATTATTCT TTTTCTTAAT TTGTAACCCG	250
40	TTTCTAATTT TCTCAATTAT TCGCCTTTCT CAACCCCCCT CCTTCCTCAT	300
	TAC	303

476

(2) INFORMATION FOR SEQ ID :940:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :940:

ACACTATTTT CAAAATCCA AATAAAGTG CAGTTTCAGA CTTTTTAAAA 50
15 AAACACCGTT GACCTGTCTT AGTTGTACAT TCAGAAAATG TAGCCTCGAG 100
CGTTTGCATG CAACACTGCA TATTTTTTCT AATCAGATTA ATATGAGTTT 150
TAATGTTT TAG CATGAACTAC AGCTAAGGAT AAAAATTTTA AAGTAGCTTT 200
20 CATAGTCTAG ATTCCTGGTT TCATAATGCT TTATGTAGTA CATTTCAGTT 250
TGCTTTGCTT TGTGGAGACT TGC GCGTATT TTCTTTGCT TGT TTGTTTA 300
25 TCGCCAGGCA GCGCTGTTCG AACTGTGAGA 330

(2) INFORMATION FOR SEQ ID :941:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :941:

TTTATTTTCAG ATAATTTTAT GTAAACAAAT TAAGAGTTAT TCATTCAAAT 50
40 TTTTGGCAGT GTTAATCTGT AATGATGAC TTGATGTACA GAAAATGCAT 100

477

TTTTGCT

107

(2) INFORMATION FOR SEQ ID :942:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :942:

15 CCACAGCATA CACACCTTGG AAACCAAGAA GACTCTTTGT GTGTGTATGT 50
GTGCGAGACT GACGCGTCTC TACGCGCTCT ATGGGGGGAG ATTTGGTTAT 100
TTCGGCGTTA CACCTCCGGT GTTCTC 126

20

(2) INFORMATION FOR SEQ ID :943:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :943:

ACTGAACAGC CGCTGGTTCC AGAACAGGCA CAGAAGGCTC CAGCGCTAGA 50
35 AACAACTGGC ACAGGAATGG TAACAATAGT CTGGCTCAGC CACAACAGGA 100
GGCTCCGGGA CAGTCACAAC CGAGAGCTTC CAGGACAGTT ACAGTCTGTA 150
AGCTC 155

40

(2) INFORMATION FOR SEQ ID :944:

478

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :944:

10

CGTGAGGAGC AGGTACCATT TTTAGTAGTC ACACAATTCC ACCTCCTGTT 50
TTTACTACTG GCAACTTCTA CTTGAGAATA ATGTTCTGAA AATGGAGGTG 100
GGGGGGGGTT TGGAAGCAAA CACATTTGGG GTTTTAAACC AATTGTTAGG 150
TTCTTTTAT TTAGGGTTGT GCAGGGAAC GTTGGGAGGT TTCTTTAGGT 200
GGGATGGGGG GACTGGGTGT TGGTTTTTGG GGGGTTTTTG GGACGGGTTT 250
TATTTTGTCC CTTAACTTGG TTTGTTGGGC AGGTGGG 287

20

(2) INFORMATION FOR SEQ ID :945:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :945:

35

ATCATTGATC AATGATATGG TTTGGATTAC TGCCCCGCCC AAATCTCTTG 50
TCCAATTATA ATCCCCAGCA TTGGAGGAGG GGCCCGGTGG GAGGTGATTG 100
GATCATGGGC ATGGACTTCC CCCTTGCTGT TTTCGTGATA ATGAATTCT 149

40

(2) INFORMATION FOR SEQ ID :946:

479

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :946:

10

TTTAACTGC AAATAGTCGT TACAAAAGT TTTNNNNNTT CTTTAAATA	50
AATTTACAC AAAGAAAGAG AAATAGAAAG CGACGGTAGT GACCAGCAAG	100
AGGAATAATA ATTACATTCA TCTTAATGTG TGTGTGCCAG TTCTGTTTAC	150
ATTAACATTG GAAAACCTCA GACCTGGACA CCAGAACCTC AAATCTGTGA	200
GTGGAATGTC TTGAGATGGG CACGCTGGAA GTCAAAGGGT TTCTCTTTT	250
TTTTTTTCCC C	261

20

(2) INFORMATION FOR SEQ ID :947:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :947:

35

CTTTAGGAAC TGTGAGCATG TTGTTGTTGA AGTGTGGAGT TGTAACCTG	50
CGTGGACTAT GGACAGTCAA CAATATGTAC TTAAAAGTTG CACTATTGCA	100
AAACGGGTGT ATTATCCAGG TACTCGTACA CTATTTTTTT GTACTGCTGG	150
TCCTGTACCA GAAACATTTT CTTTATTGT TACTTGCTTT TTACACTTG	200

40

480

TTTAGCCACT TAAAATCTGC TTATGGCACA ATTTGCCTCA AAATCCATTC 250

CAAGTTGTAT ATTT 264

5 (2) INFORMATION FOR SEQ ID :948:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :948:

CCTCGACTTA CCACGGGTGA TCCAGAATG GACTATCAGC GGTGTTTGA 50

GCCAGGTTGA TTGAGCACTG GGCTCCAAC TATTGTTAAT GAGAAACGGC 100

20 CCAACTTGA CCATGACTTT CCCATTTGCA GGTCTTAGAA TAATTTTTT 149

(2) INFORMATION FOR SEQ ID :949:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :949:

35 CGCTCAGGGT GGAAGTGGCC GGGCGCGTCG AATGTGCCGA GCTGGTGCGA 50

GTGGGCGAGC AGAGCGCCTT GAGGGTTGAG CATCTTCTGG ATCCAGCAGA 100

GGCCTCCCAG GAGGGGAGCC AGGTGGCTGA AGGCAAGCAC TTTNNNNAGG 150

40 TTCTAGTCCC CTTTTTAGAT CCTAGGGGAC TGGAGATTG GCACCTTCCC 200

481

CCAAGGCTTG GCCTCGTGCC CTATAGGGTG CCCCCCTCTC TT

242

(2) INFORMATION FOR SEQ ID :950:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :950:

15

ACTCTGCCTG CACTATAAAA TGAACCAAGG AGGATCCAGT TTGCTGTCTG

50

CACTGACAGA TTTACAGACA GGAAACAAA GCCTTACTTA CCAGGAATCC

100

AAAGTTTATA CATGAAAATT TAAAAGGGA GTCTATGCAA AGCGGAGTTC

150

20

AGG

153

(2) INFORMATION FOR SEQ ID :951:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :951:

35

TGCGGGAGTC TCACTGGGGG GGGGACACCT GTGCAAACGC GTAACGCAGG

50

TTGTTCTTAA GCGGAGCTCA GGGAGGATAC AGAAAACCTCT CCTGTGGTGC

100

TATGAAATGT GGCCTAAAAA GCATTCTG

128

40

(2) INFORMATION FOR SEQ ID :952:

482

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :952:

10

GTTGGAAATT TCCCTCAAAT CACCTACCGA TTACCCTTGA TTTCCCTTTG 50
TTTTTCAGTTT CTCAAAACGA ATGAAATAGA ATATAGCAGA ATGTTAACCC 100
ATATAAAAAT AAAGTGTACC CAAATATTGT AATGTATATT GCTGCTCTTC 150
TTCAAATTAA ATAAGGGTTT AAAACCACTT AATTGGTAAT ACAACATCTC 200
AATTGATACA AAT 213

20

(2) INFORMATION FOR SEQ ID :953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :953:

GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC 50
TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT 100
TCATTATTTT TTTTCTCTAC CATCATGTAG GCATACTCAG TGTAAGTACTAC 150
CACAATCCTG GATACCTCTC TGCTTAGATT TACAATCTCT GCTAAGATTT 200
GCCACTGCAG AAAGTGTAGT ATTTTCACTA CATTAT 236

40

483

(2) INFORMATION FOR SEQ ID :954:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :954:

GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC 50
15 TGCAGAAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT 100
TCATTTTTTT TTTCTCTACC ATCATGTGAG GCATACCCAG TG TAGACAAC 150
CACAATCCTG GAAACCTCTC TGCTTAGATT TACAATCTCT GCAAAGATTT 200
20 GCCACTGCAG AAAGTGT 217

(2) INFORMATION FOR SEQ ID :955:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :955:

35 AGCAGCGACC GCGCTCACTG GCTTTTTGTT TCTGCTTGGG CCTTTTCTGT 50
TCAGTCCATG CTTGAACTAC TCCACCCCCT TAAATCCAAC GTAAAAACCA 100
GTCTTTTCTG TGCTTGTTCT CTGTGCGTTA ATGCTTTTTC TTATGCTTGC 150
40 TTATTGAAAT ACTGTATTTT CATTGTCCCC TGGCCAAAAC ATCTGAGTCG 200

484

TGAAACCATT TTAGATACTC TACTTTCTTA CTGTGTTACG TGGCATTTTA 250
TGCTTG 256

5 (2) INFORMATION FOR SEQ ID :956:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :956:

CAAGCAATTG AGAGACTTTT TTCCTGTTAT TTTTCTACCA TTTATTTCTC 50
ATTCATTAT ATTATGGTCA GAGAATATAT TTTGAATGAT TTCATTTATT 100
20 AATTTTAAAA AATAACATTA AAAAATTTTT TAAAATGTGA ATATACCACA 150
ATACAGTATA AAGATTGTAC ATTCTGTTTT TGGACAGTTT TCTA 194

25 (2) INFORMATION FOR SEQ ID :957:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :957:

ATCTATTTTT CTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA 50
ATAACCTAAA AAAACATGTT TTCTCCACAC TAATTTTAGG GTGAATTCCT 100
40 CATTCGCTT TTCAGATCAT GGGGTGAGGG GGATGGTTCG TGTGTGTGAG 150

485

GAACTGAGGA ATCAGATGGA AAACAATGCC TCTGCTCCTT TGAGTA

196

(2) INFORMATION FOR SEQ ID :958:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :958:

15

GCGCTCAGCT GGAACTTCCG ATCTATTTTT TCTTGGTCTC ATACTCAGTT

50

TTTTTATGTA GTCACCTAGT AAAATAAACC TAAAAAATAA CATTGATTTT

100

TTCTG

105

20

(2) INFORMATION FOR SEQ ID :959:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs

25

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :959:

GACAGCGACC GACACTCAAT GGAATCCCGA TTCCATGGAA ATGGAAAATA

50

35

GCTCTATTTA TACAGCAAAT TCAAATACAG TAGCTTGCTA AGCAACTTCA

100

TAATTCATTA ACACTCGATG GCAGAGCAGA TAGTCACAAT TACTAACGAT

150

TATCATGATC TGCATTCTTG ACAAGTATAC TATGGCGAGA TAAATCAAAC

200

40

TCAGACGATG ATAAGCAAAC TCAAAAATGA AAATGATGAT GCCAACTAAG

250

486

CTTTTGTAA A

261

(2) INFORMATION FOR SEQ ID :960:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :960:

15 CACAGTTTTG TTGACTAAAC TCTACAGAAG TCAGGTATTG GGAAGGAGAA 50
TCGTTTCTTC TTTAGAGGAG TAGGTTTTAA CCATGTTAAA TTTCCAAGAA 100
TAAATTTATT TATCACCTCT ACACAGCGCA GACCATTTC A GAAAATAAA 150
20 TAATTTTCGA TTCAAGTACT ATACAAACTT AACGATGG 188

(2) INFORMATION FOR SEQ ID :961:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :961:

35 ACTTTCGCCT ACCCGGAGAG GCCCAGAAAA TTGACCAGAT GATGGAGGCC 50
TTCACCCAGC AATACTGCCT ATGCAACCCT GGAGCTTTTC AATCCACAGA 100
CACACGCTAT GCACTGTCCT TCGCCATCAT AACGCTCAAC ACCAATTTCT 150
40 ACAACCAAAA AGCCAGAGAC AAACCTGACC TAAAGCGCTC C 191

487

(2) INFORMATION FOR SEQ ID :962:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :962:

CCAAGGCAGA GTTTATTAGG TTTATGCTTT ATATTTATAT ATAAGGTTTT 50
15 ATTCATGTTA AAAACTTAAA ACCAACGGAT TATGCAAAGT GATAAGTGTA 100
TCAATGAATA TACAACTGAC TGGATTTTAA ATATACACAA ACCAGTATAC 150
CCCCAGTACT TAAATGAAGG CACTCAGTAT ACACCAAAT T 191

20

(2) INFORMATION FOR SEQ ID :963:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :963:

AGCAGGCCAA AAGCCCAGGT GAGGCCCAGC AGGAACAGCA GCCCAATGCC 50
35 TCCTAGCACT CAAGATCCAC CATAGTCCAA GCAACTGCAG TTACTTGA 100
GTACAAATAC GCTCCCGACA GCCTCATGCA GCGACACCCT AAAGGACACC 150
CGAACACCAT CAATAACCGA ATAGACTA 178

40

(2) INFORMATION FOR SEQ ID :964:

488

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :964:

10

ACTTTGCAGT CCTCACATCA CAAATAGAGT AAAAGATTCC CAAAAGGAAG 50
GGGATCCTTT TGACTGCCAG ACGCGGGAAG GAAAGAATGA AATTAAAGAA 100
TATCCTTTTA AACACACACC TCGACACAAT TTTCCACTCT GCTAAGGGAT 150
CACAAAGACT AAGACGCGGG CAGACTCCCC ATAAGCCACG CTTATAACC 199

15

(2) INFORMATION FOR SEQ ID :965:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :965:

30

ATGGAGCAGG ACCTGCGATG TTCTGATGGA TTATACCCAC AGTGTATTTT 50
GGCACATCTG CCAAAGCTA CAAACAACCC CTAATAATTA CACACTACAG 100
ATAGTGAGAA GCGTCCTACC CAGGAGTCCT GAATGTGATC TGAGTATGCT 150
CTAAGGCAGC CCCAGGAAAA GCAATCCAAT CCCTTTCTCC TCGCCTTTAA 200
ACCTGCAGGT TGGGGCT 217

40

(2) INFORMATION FOR SEQ ID :966:

489

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :966:

10

ATTTGCGACC AAAATCATCT GGGTTTATAT TTGAAAAAAC CTTGTTTTC 50

AATTTAAAAA TGCCAAGAAA GTTGTGAATA CCGTTCATTA TCACTAGGAT 100

15

CAAGAAAAAG CAAATGGTTT AAGTTTTTAC ATAGGAAATC TAAGAACTAC 150

TCATCAATAA AACGCAACAC TATCA 175

(2) INFORMATION FOR SEQ ID :967:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :967:

30

AGGGGTTTCAG GCCTGGAGTC AGGGAAGAAG GGGAAAGGGG CAGATAGCTG 50

GGGGACAAGG AAAACCTGGC GCCCCCACC GCGAAAAACA CA 92

35

(2) INFORMATION FOR SEQ ID :968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

490

(xi) SEQUENCE DESCRIPTION: SEQ ID :968:

5	GTAATATTAG GGACATGAAT GTTAGTACAG TAATTACCAC ACATGGAAAA	50
	TATTGTTCAG CAGGAAAAGT AAAACTTTCA AAAAATTCCC TAAAGATCCT	100
	ATTCAATAAA CAATTTTAGA TTTAAGGAAC CACTTACGCA AACTCGAAC	150
10	AAATAACCGA AACTCCACC TACCGCGCAA TACTCAAAAA CACAAAATA	200
	CTACTAAC	208

(2) INFORMATION FOR SEQ ID :969:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :969:

25

	AGTGGTTGGT GTTACTGGA ATCTGTGTTT TTTTTTTTCG GTTTTTTTGA	50
	CTACTCGGGG GGTTTTCCTT TTTTACAGGA ACTAAATCAA CAACTTTTTT	100
30	CGATTCCTCA ACTTTAGATT TTTATTTTTT TTGATTACCA TTTACTTTTC	150
	TTCATTTAAA ACTTTTAACG CCTCAGCCTT TTTCTTAGGC CAAGGCCTTC	200
	CACCAAGGAT TTAATCCGGG ACGGATCTAA CTGGATTTTC CGAGGTGGGT	250
35	TTAAGA	256

(2) INFORMATION FOR SEQ ID :970:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid

491

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :970:

	AATCTATTTT CCTTGGTCTC ATACTAAGTT TTTTATGTAG TCACTTAGTA	50
10	AATAACCTAA CCCGCTTGTT TTTTCCACAC TAATACTAGG GCGAATTCCT	100
	CATTTTATTT TTAAGATCAT GGGGCGAGGG AGATGATCGC GAGCACGAGG	150
	ACCTAAGACA TCAGATGAAA AACAATGCCT CTATTCCTTC AAGTATAATA	200
15	AATGATACCC GAGAGTAAAG AGCTACACTT CGCACCTCTA	240

(2) INFORMATION FOR SEQ ID :971:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :971:

30	ATCTATTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA	50
	ATAACCTAAT CCGCTTGTTT TCTCCACACT AATCCGAGGG TGAATTCCTA	100
	ATCTAGCTTT TCAGATCATG GGACGAGGGA AATGACCGCG TCGCGAGGC	150
35	CCTAAGGAAT AACATAGAAA ACACCGCCTC TGCT	184

(2) INFORMATION FOR SEQ ID :972:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

492

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :972:

	GTGTTCTCTA AGGTGATACC TTTTAATTTT GAAAGACTAA ATAATTTTAA	50
10	TCGAGAATTT CCAGTCTTTC AGTCTGATCT ATTTAATTCA CTA CTGTTA	100
	CATAATCCAG TGAAAACTCT ACTTGTGAA ATTATGACAT AAAGATCTTG	150
	CAGCTTTATT TGAGTATTTG TTCTTTTGTG TAGTTTCCAT CTTTTAAAT	200
15	ATTTAAATA TTTTCAAGGA TAAAAGTATT ATCT	234

(2) INFORMATION FOR SEQ ID :973:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :973:

30	TTTTCATCTA AAGGAGAGAG GCAGGCTCAG CTCCTGAAGG TCGCAGAGCC	50
	TCAGTAGTCC TCCTGAGTGC GTCTAACTAA CTACCATCAA AAAACAAACA	100
	AAAAAACAT CACAAACTG AACTGCCGCC ATCACCATA CACCAAGTAT	150
35	GTGATTGAAT TATTCAATGA TCTGTTTTTCG CGGTAGTGAC CAACANC	197

(2) INFORMATION FOR SEQ ID :974:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid

493

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :974:

	AGCAGGAGAT TTTTTTAATA ATAAACANCA ATGGAGAGGT GGAAATAGAG	50
10	ATGGAAAAAC AGGATCAAAG GAGCAACATA TCCAGTGA CT TAAAAAATA	100
	ATCACACGTG GCAAGAAGTT TTCTAAAGTA AACTGTATGT GGGGAGAAGC	150
	ATACAGAAAA AAACGAAATA CATAACCCCC CAGGTTTGAA AGAAAATAAT	200
15	TTTGAGTTGT ATCAATCTAT CGATATCAAA GAATGAATGA CCGC	244

(2) INFORMATION FOR SEQ ID :975:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :975:

30	TTTTTTTTTC TGAACACTTT GCTTCACACC TTCTCATATT CACGGTTATG	50
	AATTCTCCTG ACTATATCTA TTGTAACCCA AAACAGCAGA CTGTATTTAG	100
	AGACCCATTA GAGATTTTCAT GTCTATATGC CCAGAGCCTG ATATAATGCC	150
35	ACCTTACTAT ACACATAATA TAGAATCTGA GGA CTACGTT AACTGATACA	200
	TGTTAAGTAT CCTGCAGAGA GCTGGCACAT TGAATGTGCT CAATAATCGT	250
40	TAGCTTTAAG TATCTACCTC AAAGGGCTAC TGTGTGACTC CAATGAGATA	300
	ATGTGCAATG AAGGGTTTCG TGTAATATTG	330

494

(2) INFORMATION FOR SEQ ID :976:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :976:

TGGTGAAAGG AATAAGCAAC TCAAGGTAAA TAAAGAAGAA AGATGAAGAT 50
 15 TCTTAGAATC GTAGAAAGAC TGCAGGGGGA AATAATTAAA GCAGCTTTAT 100
 TCCTTACGGC ATTCATCATT CGTCGAGCTG GAAAGCACTG ACAACTTTGT 150
 AATGAGTTTT TTGCGCTTAA CTCTGTCAGG TGATTTATAT GAATNACTTA 200

20

(2) INFORMATION FOR SEQ ID :977:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :977:

AAAGGACAAT TTAATATAAA TCTATGTTTG TGCATTTCTG ACAGGCCATT 50
 35 ATTATCTGCT TTGACAAAGC CTTTCTGAAA CGCAGTGTAC AATGAATCTT 100
 AATGATGTTA TGAAACGAGC TTTGCT. 3 GCTCTTGATT GGAGCTTCCG 150
 GTATGTGATG ACGGTATGTC ATGTATGCAT GGATGTAC. 3 AACTGTGTTT 200
 40 AATACTCTGA ATTTTAATTA GAAAAAATA CAATAGCAGC AAGGCCCTGG 250

495

TTTCTAAGCT GCATACTTTT ACTAACGCGG GACATGAGCA AATGCC

296

(2) INFORMATION FOR SEQ ID :978:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :978:

15

GAATCNCGCC TGACACATAG AATGCATAAA CGAGGGGGGT CCTTCTGCAG

50

ATACTCTAAT CACTACACAG CTTTCTCTAT AAAACTACCC ATAAGCCTTT

100

AACCTTTAGA GAAAAATGAA AAAGGTTAAT GCTTGGAAGC CGGGGGAGGA

150

20

CTGACCACTT CATAAGCCAG TACGTCTGAG CTGAGTATGC CCCCAGAATC

200

CAGCCACTAC TGATAATTCA CAACGGTA

228

25

(2) INFORMATION FOR SEQ ID :979:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :979:

CGTACAAAAG CGCTTTGGAG ATGCCAGAAA AAACCCTACG GGAGGGTTAT

50

CCCCCTGACG CTAGGCCATG ACACAATAA ACTTCAATAC ACCAGGACTA

100

40

AGGCAAGTAT GAAGAAGCAA AATATCGTAA CGACGCACCC TCGAGATCTA

150

496

CCAGGCAAAA CCAGAACCTG A

171

(2) INFORMATION FOR SEQ ID :980:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :980:

15

TGATTCCCCA TTTCCCTGGA CAGGGCAGAG TCAAGCCGAG AAGGAGGAGC

50

CACAGGCCAG CTGTTAATGA GACACTAAAT AAAACGTTCA GTATTCATAC

100

CTGTGGAACA TGGGTGAACC TTTCTGGTAA CTCGATTTTT CACACCAATG

150

20

ACAGCAAATG AGAAAGTGAG AGAAGCTAGA TAAATGTTTT TAAAGCATT

200

CTGCAGTGA AAATAACTGC ACTCTCAGGA CACAGCACTG T

241

25

(2) INFORMATION FOR SEQ ID :981:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :981:

TCACTGCAAT CACGGTAGCT TCGCCCATTG CCTCTTCAAC CAGGCACATA

50

CATCGAGAAG TTGAACCTGC ACTTTATTTT AACTGAACA GACTTACCCC

100

40

GACAACAACA CCTCCCCAGT GGGACAAACC TACCCACCT CCCCACACTC

150

497

TACTCCCAGC TAACGTTCCC TATAATCATC ATGACCCATT AAACATTTGC 200

AAAACCACAC TTCAACCCAC AGGAAGA 227

5 (2) INFORMATION FOR SEQ ID :982:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :982:

CGTTGTCGCC ATGTAATAC CGCTCAGTAC GGGAGGACCC ACAGGCTAAG 50

20 ACACTCGGAG CACGAGCTCG CCTGAGGGAC CAACGAGGCG AAGCCACAAT 100

CCGCGAACTC ATGACTGACC CTTCTAAGT AAGAATCCCA CCCAGGCAAA 150

CCAATCCGAC AACCGAAATA GCGCAGGCAC CGCCAAATTC AAGGCGCCCC 200

25 AAAAG 205

(2) INFORMATION FOR SEQ ID :983:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :983:

AGCAACCGGC ACTCAAGTGG AATCCCGAAA AAGTGATTTA AAAATGATCT 50

40 TACCTGTACC AGAAAAGCAA AATTAAAGGA AACAAAATAA GAACCATAGT 100

498

CCCAAATGAC ATTTAACCGT ACATACAGCG ATAACATGTT CAAAATCCAA 150
CAAATAACGC AACTTCCAGA CGTAAATATC CGCCACTCGA TTCCCTCCCC 200
5 CCCT 204

(2) INFORMATION FOR SEQ ID :984:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :984:

ATTTGTATTA GAAAAGTAAA GTTGAAGGAA ATAAAATTG CATTCTTGTT 50
20 TTAAGTGATC TTTAATTGTA TATATCGCGG TAGTATGTTC AAAATCCACT 100
AAGTACTGTG ACTTTTAGCT GCAAATCTTT GCTCTTTGCT TTTTTTTTTC 150
25 TTTCTCCCCC CTCCCCAG 168

(2) INFORMATION FOR SEQ ID :985:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :985:

CTCAGCTGGA ATGTCCGGTG CCTGCTAGGT GCATGGCCAG AGAAGCATGG 50
40 GCTGGGCCTG GGCACAGGAG GAGCAGCTGC TTTGGTCGGG GTGGAGACTT 100

499

TTTTTTTTTT TCTACCCACA GCCTATTCCA CTCCTCCCCA TCTCCAGGCG 150
CTGGGAGGGG GGCCCTCACC CCGTCACGCC TCGCTCCCTC CTGGCCCTCT 200
5 GGTCCAGCCC CTTACGCCTC CTCTCAGTCT ACTCAATTGT GACTGTCCCT 250
CCTGATGTAT TTTTTTTTCC TCCAACTCAA AAGGCAAAAA TAATCCTATT 300
TTTATTATCT TGCTACAACT GCAACTTTCT GCCCTATAAA TTTACATTCC 350

10

(2) INFORMATION FOR SEQ ID :986:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :986:

AGCGACCGCC ACTCACTGTG AGTTCCAATT AATTCAGGTG AGCCGCTCTT 50
25 CTGCACCTCC TCCTCACACC TCTCTACCTA TACTAACCAT TTTTGAAGGT 100
TCAACAATGC TCTGCAAATC TTTTAAAGAC CCGTTACTTC AACAACTCCC 150
AATACCTTCC TCCTCAACGG AACAACTTAA CCGTTACCTT TTAAACCCGA 200
30 CGAGCTACAA AGCAAGAGAT ACTTCGCGAG CCAAATTCTA CAAAGGACCA 250
AAAAAGAAAC CCATTACCTT ATAGTACTCA TGCAAAAAA 289

35

(2) INFORMATION FOR SEQ ID :987:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

500

(xi) SEQUENCE DESCRIPTION: SEQ ID :987:

5 CACAATCATA GCATTTATTA CACGATTTAC ATCTGATCCT CACGCAATTT 50
TCTTCCTCAC CAATAAAGAA CTAATAGGAC AGCATATTAG AAGCAACATA 100
CATTCTTTTA TTCTTGCATC GCTATAAAGA AGTA 134

10 (2) INFORMATION FOR SEQ ID :988:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :988:

TTCTGAAATG AAGGTTTCGT CTTAGCTAT TGACTGTAGG ATTTGTAATT 50
CAAATCATCA CAGCATCCTA AAGAAATACT GTGTGAATGG AATGCACACA 100
25 ATTCCTACAG AACACACAAA CTGATGTCCA AAAGGCACAG AGTAATGCTG 150
GTGGCTCTTT CTAGTCAGTT AAGAAACAAT AAAAAGTCTG CATTATTCTT 200
30 TCATAATTTA AATACTTAAG TAATCTCCAC TTTATTATTT TATAACAATG 250
ACTTCAAATT TACATTATTT TAAGTACCAT TGTAATC 287

(2) INFORMATION FOR SEQ ID :989:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

501

(xi) SEQUENCE DESCRIPTION: SEQ ID :989:

AGCAACCAAC ACTCACTGGA ATCCCGCAAT CAAGAGCTAA AAGGACTTCT 50
5 TCCATCTCTC AGGGACACAC ATCCACCGAT AAGAATAAAA GAAATGCCTG 100
AATGACTCTC ACTGGCACTT TTAAACACAG CAAGCCCAAC ATATTTTCTC 150
CTTTTCATAA AGAAGCCTAT ACACCAT 177
10

(2) INFORMATION FOR SEQ ID :990:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :990:

TTCCTATACT ATGTCGGTTA AAAGCCTTCA TAGAATATAG GCACCAAAAA 50
25 TAAACTAACC CCACACCCTC ACCAACCAAA GGAGGCACAA TCCAACGAAA 100
CTGATGAAAA GTCGAGGTAA CGACTCTGCA GACCGTACTC ATTTCTAAAC 150
CAAAAGTC 158

30

(2) INFORMATION FOR SEQ ID :991:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :991:

502

	TAATCCCTTT TAAGCAGAGA TACACATTCA CAGAGAGAGA ATGTTTTTAAA	50
	AAGACCCACA AGGGGAAGGG ACCAAGTAAG CACTTTTAAT TCATTTTGAT	100
5	TACACAAAAA TAAGGCAAAC TAAATGATTC AGAACAATTC AATTAACTG	150
	AAGCCTTCTA GAAAATACT CAACAGGCTT CAACAAAAG ACTTAGCGCA	200
	CATAAAACAA TCACGAAGAT CACAATTTC GCACAAATAT CTGAAGGAAT	250
10	ACACGCAAAA CATCATA	267

(2) INFORMATION FOR SEQ ID :992:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 199 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :992:

25	AGGATGTGTT CATGCTGGCT TTCAGGATGT CCCAAGGCAC GGCACAGTGA	50
	TTGTCAAATT CCACTTTGCA TGGAAGACAG CACAGAACCC TGCTCTGCGT	100
	CAGCTGGAGA GCTCCGGCCA GCACGGCCAC CAGCAGCATG ATCAGTGTGA	150
30	TGCAATACCA GAAGCCGTCC CACCATGATT TTAAGATGTG ATAAGATGA	199

(2) INFORMATION FOR SEQ ID :993:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 198 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

503

(xi) SEQUENCE DESCRIPTION: SEQ ID :993:

TTTAAGGTGC TAAACTTGCA CCTCATGTCC ACTCAGTAAC AAGTATTGGG 50
5 ACGTAGAGCA CAGCCTCACT CAGCTCTGAA AGGTAATACA GCTTGCGAGG 100
AAGTGAGCCA GCAGTGGCCT TTGCAATTGT GGATCTTGAG CTTTGCTCTT 150
AGCAGATCTC AGGCGTAACC ATTCGCTAAC TGTACTGAAG ATGCGTCC 198

10

(2) INFORMATION FOR SEQ ID :994:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :994:

GCTATCTGCG GGGCCATTCG TAGGATGGGT GAGTCAGATG ATTCCATTCT 50
25 CCGATTGACC AAGGCCGATG GCATCGTCTC AAAGAACTTT TGACTGGAGA 100
GAATAACAGA CGTGGAATAT TTGTCATAAA TAAATAACGA AAACCTAAAA 150
AAAAAAAAA ACAACAAACC CCAACAACT CAA 183

30

(2) INFORMATION FOR SEQ ID :995:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :995:

504

ACCTCTGCAT TAACTACTCCA GCACCTTTGG TTAGCCAATT TGGCCTTATT 50
TGTGTCTCCA CCATTGGATT ATCTGTCCAT CAAGGTCAGG AATGTTTTTCG 100
5 GGTTACCCCA CTGTCCCCAA CTTTGAATAT GCTCACTGCC TGGAAAATGT 150
TTATCTGAAT ATAAGGCATC AAGCCAGAAC TTGCCCAAAA CTAAATCTA 199

(2) INFORMATION FOR SEQ ID :996:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :996:

20

GGTCTTGGCT GGTGGTTTAT GGCCCGGGCC TTCTTTCTAC GGGGGCCAGG 50
GTCCAATTTT CCACCTGGGG TTAAAAGTT AAGGAGGACC AGCCTGGGAA 100
25 CCCCTCGAGT GGGGACGCCA TTTCTATTAC CAGGGCCCCC TTATATTTTA 150
AGGGGACACC ATATGGAGAT TTTATGC 177

(2) INFORMATION FOR SEQ ID :997:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :997:

40

GAGTTTCCTG TGCTGTTACA AATGTAACAT TCTCATATAC AACATTCATT 50

505

GAAGAGGCAC AATTCTTATT TTGAGGTGGC ACAGATTAGA CAAATTTTTC 100
AGTGAATAAT TCCTCTTTCA TTAGGAAATT TAACCACAAG CTGTATTTTC 150
5 GTAGAAAGTT GCTTGAAATT CTTTTCCTAA AAAAATTAA TTTTCTATC 200
TCAAATGAC CGTATGCAAA CGAACATTA 229

(2) INFORMATION FOR SEQ ID :998:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :998:

20

TTGCAGTGTT TATGCCCCGCC TTCTTTCACG GGCAGGTTC AATTCAGTGG 50
TTTAAAAGTA AGAGACAGGC TGAACCCTTC GTGGAGCCAT TTCATTACAG 100
25 GTCCCTTAAT TTAAGGAACA AGTTGATTGA TGCTACCTTT TTGCACGGTT 150
TAGGGTACCG CGGCCGTTAA ACATGTGTTC ACTGGGCCAG GCGGTGCCTC 200
TTAATATCCG GGGATGTCCA GAAGGGGAGT TTT 233

30

(2) INFORMATION FOR SEQ ID :999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :999:

506

TCAAAAACCTC AATATAATAT GTAAATCAGG GGTGTCCAAT CTTTGGCTT 50
CCCTAGGCCA TACTGGTGTT AGGCCACATT CAAAGCTATC CTAGGCCACA 100
5 TGTGGCTGGT GGGCCATGGG TTGGACAAGC TTGATGTAAA TAAACCACC 150
AGTGGAAGA GTTTGTTGTG AGTTACATTC AAATACAACA GGAGTAATAC 200
TATCATGATA TTAGTT 216

10

(2) INFORMATION FOR SEQ ID :1000:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1000:

GACAAGACCT AGAAGCAACA ATGCCAGTA GAAACAAACA CACCTACTGC 50
25 CTGGATCTTA GTTTTAAATT ATATCCCCA ATAAAGAGAC CCAGGGCTCC 100
TTGTTGAAAT GGCTGATTCT AGGACTGGGG CAGGAAATAT GCAAGATGAA 150
CCTAGAATAT CTAATACTGC CAAAATTAA GAAAGTGTTT TAAAAAAAT 200
30 CCCACGGAT AGGGTGTCAA AAGAGACATA GAAGCCATCT GAAGGAGTTC 250
CCAATGGCCA AAGATCAAAT AATTTTCAA 280

35

(2) INFORMATION FOR SEQ ID :1001:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

507

(xi) SEQUENCE DESCRIPTION: SEQ ID :1001:

5	TGCATGATAG GAGCGTCCTT TGTTCTCATG AGGTGACTCT TGGTGGGCTC	50
	CTTATTTGGG GACTGGTCAC CAAAAATACC TAACTATGGT TGGAAGCTTA	100
	GTGCTTTCAG CCCCATTCCC CATCCTCTGG AAAGGGGAGC AGAGCTGGAG	150
10	CTCGATCATG CCTGCGTGAC AAAGCCTCCA GAAAAATCCT TGAAAGACAG	200
	GACATGGAGA GGCTGCTGGG TTGGCGAACA CAGCCATGTG CCGGGAGGAT	250
	GGTGCACCCC AACTCCACAA GGACCCTTCC AGACCTCACC TGTGTATCTC	300
15	TTCATCTGGC TGTTCATTTG TATC	324

(2) INFORMATION FOR SEQ ID :1002:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 254 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1002:

30	ATTTCCATTC ATAAGTCCTC ACAAACCCAC TTTTCCTCTT GCCTGAGTGC	50
	CTCACATACC CTACTGCCTG AGATGGTTCC AGAGGCGGTC TCCTCTCTCC	100
	CCCAACGAAA CACCAGGCAC ACACCTGCCC CCAGTCTTGC CTGCACTCTC	150
35	CTTTCCTCCC GCAGAGAGGC ATTCCTTTCT CCTCCTCTCA TCCTACACAC	200
	ACTATAAGAG ACAACTGAAA TCTTGCTTCC TCCAGCAAGC TTCTTAATTC	250
40	ATTT	254

(2) INFORMATION FOR SEQ ID :1003:

508

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1003:

10 AAGGTTGCGC TGCCCATCCT CTCGCCCTTC GGAATTTACC CCTGGCCGCT 50
CAGGGTCTCG CTTCTAGAAG AAGATGATGG ATACTAGGGC GATCCTCCTA 100
15 TTGCCTTTAT ATTTAACAGG CCCGCCGAGG AGGGGCTCCC GCTGGTGCCC 150
ACATAACTCT ATTAGACCAT CTGAGGCGAC TTCCCCCACC CCCTCCAACG 200
CGCCTCACGC ACGACTCTAG CAAAAGACAG GTTCCGCGGT GGTCACGTCG 250
20 TTTGAGACTA TACTG 265

(2) INFORMATION FOR SEQ ID :1004:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1004:

35 AAATATGCCC TGAGGATTAT CTGATGTCGA TGGTGTGGAA AAGAACTCCA 50
GCAGGCGACT TCGATTCAA TCAATGTCCC CTGAATGCCA CAGAACCACT 100
AGCAGACGCT GCTCTCTCAG TCTTAATGGA GTGGCCTTCT GGGAACAGCC 150
40 GAGCTTTGAA AGATGCATAT CAAATGAGTA CAGACACTTG TAGCATTTAA 200

509

TCAAAGAGCA CCTTGCTAAG AGGCAGCGAA TGCTGGCAGG TGATGGAATG 250

CCCCAGGTGA CCA 263

5 (2) INFORMATION FOR SEQ ID :1005:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1005:

CGAGACTGCA GTACTTCTAG AAAGTTGTGA ACTTCTAAGA AAGAGCCAGG 50

20 CTTCCATCTC ACTATTCCTT GATCATTATC TCTGAAGTCC CTACCTGCAC 100

TTCCCTGATT GTCCTGTAGC AACACCAGCA TGGTGGGAAT TGCAGGCAAA 150

GATTGTGAAA AATCCCTAAA GGGTCATTGC TCATGACGTT ATTTCTGAATT 200

25 GTAAAATCGT GAGCCACTCA TATTCAAACCT AAAAAAAGAA CAGAACTTTT 250

ATTCACGTTG TGAAGCTTAC TCCCTCGCCA TTTTACGGAT CAATGTCAAA 300

30 CGCTTGCATT CATAAAG 317

(2) INFORMATION FOR SEQ ID :1006:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1006:

510

CGGAAGCATT ATCCTGTCAT CAGAAGATGG ACCTTTCCTT GGAATGCCTT 50
TTCCCTATCA TGTCTGTGTG GTAAATACCT ATTCATCCTT AACAACTAG 100
5 CTGAGGTCTT ACCTCATCAG GATTTGATCC CCCAAAAAGA TTTGTCCCTC 150
TCTGAGCTAT CTTTATAACT AGTACATACT CCTACCAGCG GACTATGTTA 200
TAATAATGTG GCTATATGCC TGTGATCTCA GCGTGAGCTC TTTGAGGACA 250
10 GAGTCTTTGT CTAAATACTC AAAACCCTGT TTACCAT 287

(2) INFORMATION FOR SEQ ID :1007:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1007:

25 GGGCACCAAA ATACACATCA GAGGAGACTG GCTTCCATGA GACGCTTCGA 50
CTGTCTCATC GGGGCACTTG TAATAAGCAT CTTGATGCCA CTGAATGCAA 100
TGCTGTATTG AAATAATAGC TTTCATCTTC ACTATAAAAC AATACAAACG 150
30 TAAACTTTGA AGCCCTTTGA AGGACCTAAC CAAACAACAC AAGGATGAAA 200
ATAGATCAGT ACAACTTTGA GACACATTAT TAGGTCAAAT CTGCAAAGCA 250
35 TATTCGGATT TTACCGTAAG GAA 273

(2) INFORMATION FOR SEQ ID :1008:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

511

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1008:

TAGAGTGGGG GGCCAAAACC TCTGCAGTCC CCGGCAGTGA GCTATGGACT 50
TTCTTCCCCC TCACAAGGCT GGGGGCCTCC TGCTCTCGTC CCTGGCCCTC 100
10 CCTGCACAGG GCAAAGCCAG TCTGGGCTAT GGCACACAGA GTTCATGTTT 150
GCGCCCTCTC CCTGCCCTC ACCCCAGAGG GTGAGGAGGA ATGAGGGGCA 200
15 TTGATGGTTA GGCCGGTTGT TGCCTCGAAC AGCTGGAGGG AAGCTGCAGG 250
GGTGATAAAA TCAAAGCGAT ATTGACACAC TACAAACATT ATAGAACCTG 300
CAAAAAAA 308

20

(2) INFORMATION FOR SEQ ID :1009:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1009:

GAACCGCCTC TGTTTCAGA GCAACTGGTC AAAACCTCTC CAAATACCGA 50
35 GCAGTTTGA AACTGGATT AGGAACCACT AATGAAAAG AACAGACTCA 100
GGGACAAGTG TTTGGCGGGA ATGTGTGAAG AGGTAATAA TGAGTGTAC 150
TGAATCACAC TATTACACAG ATGAAACAAA GCCTTTA 187

40

(2) INFORMATION FOR SEQ ID :1010:

512

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1010:

10 AAGAAAAAGA TATTAAGATG GGCAAGTCCT GGTGGCAAGA CAAGCAGATG 50
ACATTACAGA CAATGGACAT CAAACTGCTG CCAAGCTAAT TTAGATTGTA 100
15 AAAACAGCTC CATAGTCAAT ACCCATGAGT GATCTTAAAT ACGCACAATT 150
AAGCTACTTC TCCTTGATAT TACCT 175

(2) INFORMATION FOR SEQ ID :1011:

20

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1011:

30

TGAAAAATAT TTGGAAGTCT TTAGTACAGA ACAGTTTCAA TATGAGTTAA 50
GAATCATGCG ATGACTACCA AAAAGCTAAT GCGATCCCAG GCTGCGGTAA 100
35 CAGAAGCAGA GCAGCTCAGC TGGGGAACGT GATAGTGATA ACTACTTCGT 150
ACTAGGTTAG ACTGTACCGA GAGACCTATG TTCAGTTCTG GGAGTGAAAG 200
TATTTTAT 208

40

(2) INFORMATION FOR SEQ ID :1012:

513

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1012:

10

ATGATATCTA GACTACCACT ATTTTTTGAA TGAGGCTTTC TTAGGAGTAT 50
GTTGATGCAC TCTCATCCTT TCCTCCCCGG ACTCCTACCA CAACCCTCTG 100
ACTGTGGAAT AGCATGGTTG TGTGTAAGGC TGGAGCACAG GCACAGTGAG 150
ATGAGGATGA GCGATTGAGG GATGCTATAA GCCA 184

(2) INFORMATION FOR SEQ ID :1013:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1013:

30

CTTTGACATT TGATCAGACC AACAGTGCT GTTTCCCGGG GAGGAAACAC 50
ATTTTAATAA ACACATCATC CCGCAGGCTC CCACCTTTAC CTCATGTTTC 100
ATACCTTGTT TATCAAATGA GCGACTCAAA ATGATTAAAA ATAATGCTGT 150
TCTTTAGTAG CAACTAAAAT GTGTCTTACC GTCATTTATA TCTTTGTCAC 200
CGGAAAGAAG CATTTTTGAT ACTTTACTGC GAGTCAAAAA TCAATACGCA 250
GAATGGCATT TGA 263

40

514

(2) INFORMATION FOR SEQ ID :1014:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1014:

CAAATTAAGT GCCAGAATGA TGCAGCCCGC TCTCACCAGG AAGAACGACA 50
15 TGTGAGAAAA CTTATAGCAG ATGCAAAAAT GTCAACCCAC CATGTTATTT 100
AAAAAAAAT ATGACCAGGA TACAAGGACA CTTACCGTT TTTAACCCAC 150
ACAAGGTCAG GTAATGTTTA CCTTGAAACA CAATCGCATA TGACCCTTTA 200
20 TGCCACTCAC CTAGGCCTTT AATAATGAG 229

(2) INFORMATION FOR SEQ ID :1015:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1015:

35 GAAAATAATG ATTCATATTA CCGGGTATTT CTTATCCAGT CTTTCATTCT 50
ATGTAAATTG TGTGTGTGTC TATATATGCG TGCATGTCTC TCTCTACATG 100
TATATGTGCA TATGTATGTA TATATATGCA TATGCACATA CATGCCACAC 150
40 ATGCACATAT ACACACACTC ATAGAGAACA AAATTATTCC GAATATTTCA 200

515

TGAGGTTTCT TATTATAAGG AGACAATATT GATGCAATCT AATTAA

246

(2) INFORMATION FOR SEQ ID :1016:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1016:

15

TTCATAATCG CTGGCACTGA ACAAAGTTGC AGAATTCTTT GCCAGGTACT

50

TTAGGAAATC GTGAAGATAA TTGAGTAATA AAGCAAGGCT CTTCTCATCC

100

AGAGGTGTAT AAGCCAACAT CGCTCCAATT CGTACAAATA ATCTCAGGAG

150

20

ATGTGGCGCT CCATACACCT GGGACATGGG TGCATCGGGA TGATCTGCAA

200

GAATTTCAGC ATACTGTGGT CTCTCAAATT TATAGAGTAG CTGGGTACCC

250

25

AACATTACGT TGAAGTATTC TTTTATACTC GCCACAA

287

(2) INFORMATION FOR SEQ ID :1017:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1017:

ATATGAGAAA GCAGAGCAAA ACAGATGATG CTCTAAATGC AACTGACACA

50

40

CTTGCTAAAG ACGTTAGGTG CTCCATAAAT GCTTGTTGAA ATGCTGTTTG

100

516

TCAACATTTG TTGTGAAAAA TTCATCTCTC CATCTAAGAA TCCTCATGAG 150
TTAACCACAA TCAGTTCTAC ATAATTTAAC AGAAAACATC TGGTGGCACT 200
5 TTTAAATGTT TAAGGACAGC ATTTACAAA CTAAGCCCGC CCCCAGTCCC 250
ACTGCAGCAG GAGAAAATAA GGCTATGGAG AAAAGCAAGA TGAGTTATA 299

(2) INFORMATION FOR SEQ ID :1018:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1018:

20

ATTACTCCTT CTCTCGAATG CTTCCAGAAG AGTAGCACTC ACCACCTCAT 50
GAGGAAAGGC ACTGCAACTT TGGTCAATGA TATCTGTTAG AAAGATCTTT 100
25 TCCTATATTT AGAAGAGTGA TTCTCATACC TGAGCATGTA TGAGAATCAG 150
TGGGTTTGAG GTGGGCCCAA GAATTTCCCT TTTTAACAAG TTCCCAGAAG 200
ATGCTGATGT GGCAGCTTCT AGCACAGTGC TTGAAAATCC ATGAGTTTTC 250
30 AAGAGGACAA TCTAAAGTGC TCCC 274

(2) INFORMATION FOR SEQ ID :1019:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

517

(xi) SEQUENCE DESCRIPTION: SEQ ID :1019:

TTTCTTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA 50
5 CAATTCCAAT GTTACGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC 100
GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG 150
CATCTTCTAC CACTTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA 200
10 AAATGGCACC TCATCTTTGA TCAAAGATTC AG 232

(2) INFORMATION FOR SEQ ID :1020:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1020:

25 AACAGTCCAT GCTGATCTTA GTAACATGA TGAAGATGGT GCTTGGCCTG 50
TTCTTCTTGA TGAATTTGTT GAGTGGCAAA AAGTCCGTCA GACATCATAG 100
CAAGAACTAT GTGAAGAAAA TGCAAACCTT TAC 133
30

(2) INFORMATION FOR SEQ ID :1021:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1021:

518

	TCCTAGAACT CTGCTTGGAC CAGAAGATGT GAATAAACTT AAGCTTATTT	0
	ATTTAAAATC ACAAATGAGT TGCTCTAGAT TCTAAAAGGG TGAAACTTTG	100
5	ACTGTTGAAA GTTTAAGTAT TAGTAACTT GAGTTACTTT TTCTTTCAAA	150
	TTTCACTCCG CTTCCCTGCA TTTCGAAGCT GCTCTTTCTG GTCCTACCCA	200
	CCACCCCACC AACAAGACTT GTGTTTGTTA ATAGAAATAA TTTATCAAGG	250
10	TATTGGGGAT CCATTGTCTA TATTTAAAAC	280

(2) INFORMATION FOR SEQ ID :1022:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 304 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1022:

25	AAAATAAATA ACTTCTTAGA TTTTGGACTG AAAAGATCTG AGAATGTTCT	50
	GCCAAACAGC CGACCAACTG GTGCAAAGG TTAAGGCTGA CTTGACTTAG	100
	CAACCTGCAG CACAACCAA AACACTGATG CAGTTCAGAG CTCTTCAAAT	150
30	GCATACTTCA GTGTTACACA CACATCAATT AAATTAGGTT AAATTAGTTA	200
	ATCCTCTAGA CAGTTTTCTT TTGTTTTGC ATGCATCCCG TTCCATTTTC	250
35	ATTACGGGCA TCTATTCCTT GATCAATTAT GTGCTTGCT TTTAATCGG	300
	TTTT	304

(2) INFORMATION FOR SEQ ID :1023:

40

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 237 base pairs

519

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1023:

10	TTTCTTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA	50
	CAATTCCAAT GTTACGAAGT CCAAGAAGT GGAATGAGAA AACTCCTCAC	100
	GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG	150
15	CATCTTCTAC CACTTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA	200
	AAATGGCACC TCATCTCTGA TCAAAGATTC AGAGCAT	237

(2) INFORMATION FOR SEQ ID :1024:

20

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 320 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1024:

30

	GGCATGATTA TTAGAAACTA TTTAAGCTTT TTTCTTTGAA AAACAAGCTC	50
	CTTTTACAGA ATATAAACAA CAGTAGTGCC TGTGGTTTAG CCCACCAATC	100
35	TTGATGACTA AAAGTAGCTG ATGCATTGTG CATATGATGC TTGAGATGGT	150
	TTTTGCAAAA GCAGAAATCG CTGCAAGGTA ATCACAATAG ATAAAAGTGG	200
	TATTTTAAAC CTTTGAAATA AATGGATGTA ACTGTACCTT GGTACAGCTT	250
40	TTCACTTGTT TAGTTTTTAA ACGTTAGTAT AAGATTAGGT AATTGAGGGT	300

520

TAGAGCCAAC AGGAATCTGC

320

(2) INFORMATION FOR SEQ ID :1025:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1025:

15

TTCTGGCACC ACATTCAATA CTGATTCACA GGGATCTAAA ACATTCTAGT

50

TATTCAGTCA CTCTGTCCTG TGTGGCAGAT AGGACTTATG TATCTTCAGA

100

ATATTTGAGG AGTCATTCTC AGAGTCTCTC ATGAGTGCTC AACTTAACTG

150

20

TTCCACAAGT CTGTCTTCAT AGCTGCATGT TGCATCTTCC AGTCTCTGTT

200

CT

202

25

(2) INFORMATION FOR SEQ ID :1026:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1026:

ATTGGTAGAC AATATCATAA GAGTTTCTG ATAAAAGATG CTTTTTAACC

50

CTGACTCCCA GTCACAATTT TGGCATCTCA TCCATGGGAA AAAAATAGGA

100

40

AACTTATACA TTTCATAAAC TAAAGGTCAT CCAAACACTG CCAAAAACGT

150

521

TTTTATAAAT TGAGACCTAC TTACATCACA TCGGTTTTCC AAAGAGAATA 200
CACAGCGAAA GATGAGGCTC CACCCGGCCG GCACAGTCAT GAA 243

5 (2) INFORMATION FOR SEQ ID :1027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1027:

TATTTGCATT GAGGAAATAT TAATTTTCCA ATGCACAGTT GCCACATTTA 50
GTCCTGACTG TAGGAAACAC TGATTTTGTA AAGTTGCCTT TATTTGCTGT 100
20 TAACTGTAA CTATGACAGA TATATTTAAG CCTTATAAAC CAATCTTAA 150
CATAATAAAT CACACATTCA GTTTTAAAAA AAAAA 185

25 (2) INFORMATION FOR SEQ ID :1028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1028:

GCTTCTCTAT TCCTCCTGCC CGGGAGGAGT AGAGGAATTC TGGAGCCACC 50
TTAGTGGGCA ATGGGGGAGC TCCTGATGGT TCAGGAGCAG GAAATTTATG 100
40 AGCAGAGTGG GGTCCCAGGC CACAGGGAGA TGTCTATCCA CAAGGGATGG 150

522

TGGCCAAGGG TTGAATGGAA AGAGGCAGGC AGGGGGAGAG GGGCAGAGGG 200
TGTGGGTATT CCCAGGGCCT TGAGAGTGGA CATGGCCCCT TCTCCTCAGC 250
5 CTTCCATTAG CAAGGATGTC ACTGCTGCTC TTGCCTGATG ACAGCCAGAT 300
CTGTTCACAG TT 312

(2) INFORMATION FOR SEQ ID :1029:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1029:

20

ATTATTTATA AATTTTAGTG AGCACCACCA AAGTTAGGAT TCAATTGAGT 50
TTGAATTCAA ATTCATTCAA AAGTTGCACA AATTTATTTT TTTTTCCTG 100
25 AACATTCCTT TACTTCAGAT TGACAATTCA TTCTATTTAG AGCGCTATTT 150
TAAGAAACCT TGATGAATCG CCCTTGACTA AAGGAAACAA AGTAGAATTT 200
TATACAGATG GAAAAAGA 218

30

(2) INFORMATION FOR SEQ ID :1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1030:

523

TTATTAGGGG GTTTAGAAAA TAAATTCGTA GGGTTTAAAC ATTGAATAAA 50
ACTACAAAAA AAGACACACA TTCAGGTAGC GAGGCTCTGG GGGTAACTCT 100
5 TTCTTAGTTC TTTGGACACA TCCG 124

(2) INFORMATION FOR SEQ ID :1031:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1031:

TTTTGCCAAG TATATGTAGT GCAAATATTT TCTTTCAGTC TGTAGCTTGC 50
20 CTTTTTATTT NTTAATGGGT ATCTTTAAAA AAATGGAAGT TTTAAGTTTG 100
AATGGAATTC AGTTTGTTTT TAAAGCTTGT GCTTTTTGTG TTCAACTAAG 150
25 GGATATTAGC TTACCATTTT TCTCGTTGA ATATTATGTG TTTATAGACA 200
AGAAATGGTC ACTAAAGCAA AATAACTGAA AATTATC 237

(2) INFORMATION FOR SEQ ID :1032:

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1032:

40

ACAGCAACCG GCACTCACTT GGAATCCCAG TGTTCGAGT TCTAAGGCCA 50

524

CTGAAAACCA TCAAGCGCTT GCCAAGCTCA AGGCCATCTT CGACTGCGCA 100
GCGACTTCCT TGAAGACTGT TTTAACATA CCAAAGGAGG ACAAGCT 147

5 (2) INFORMATION FOR SEQ ID :1033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double.
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1033:

AGGCCTGCCT ACCGTAGGTC TCTCAGAGCC TTTACTCTAG TCACTCTTTA 50
GAGGGGGGCA CTAGAAGCAA TATCTCCGAA ACTTCTTCGA CTGTCGAGAC 100
20 TTTTACTCA TAATTCGCTT CAAGCCAAC TACGGAGGCGC ATTTACAAAA 150
CTGAAATACG AGCGACACCC CAGGAACGCA CGGAGACATG ACGCCCTTAA 200
25 TCCTCTGTCC CTA CTCCCTC TCCTAGGACA CCGCATTA 238

(2) INFORMATION FOR SEQ ID :1034:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1034:

TCCATGNCTC NTGGTCTCTG TGCNCTTGNC AGGGGCATGC CAGGGCCCTT 50
40 GGACTGTGCA GGG 63

525

(2) INFORMATION FOR SEQ ID :1035:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1035:

CGACCGGCGC TCAATGGCGA AATTCCGAGC CAGAGCTATT GGTGAATGA 50
15 GTAGCGCTGA TGCTTTAGAT AATACTAGT ATGGGGATAA GGGTGAGCAG 100
GCGCGCCTTG AGGCAAGAAG CGGGTTAGAG CATCTCTACT TTAAAAGCCA 150
AAGCCTATAA CGGTAGCGTC TACATCACGA 180

20

(2) INFORMATION FOR SEQ ID :1036:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1036:

CCAAATACGA TGACATCAAG GAGTCGATCC GTCAGCGTGA CTTGAATACA 50
35 CCACCGCCGA CGACCCGAAA GCCTGATGAG GAGAAGTCCA GAATCAGGAA 100
CAACGGCGAC ACTCGACTAA CCATTTTAAA CCAATTGGAA CC 142

40

(2) INFORMATION FOR SEQ ID :1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs

526

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1037:

CCACATGGAG TGACCTGGGC CTCTGCAAGA AGCGCCCGAA GCCTGGAGGC 50
10 TGATTGTCAA AGCAGGGGGC AGGACCCGGG GGCAGGAGAA ACCAG 95

(2) INFORMATION FOR SEQ ID :1038:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1038:

25 ATTTTATTGT AGTAAGAATA ATACATAGAA ATAACATTAA ATAAATATGT 50
TTGACAAAAA CATAACACACA TAGTACAGGT AGAACATATA ACTGGTTGAT 100
GCTAAATAAC AGATCCAGAT AATTTTCAAT TTGAATTAGC AGCAGGGAGT 150
30 CATTGAATGC TATGCCCTTA GAATGGCTTG CAGGCTTTCA CGAGT 195

(2) INFORMATION FOR SEQ ID :1039:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

527

(xi) SEQUENCE DESCRIPTION: SEQ ID :1039:

GGTTGTCAAG AAAATGAAAG GTAAAGCTCA GAAGGGATAA GGGAAGACAT 50
5 TACAGAATTT ATCATCAAGC AGGAGGTTTT TTCCAGGTTT TAAGATGAGG 100
TTAAGTTTCT TAACAAAAGA ATAAACAACT GTGACTCTAT CTGTCGGGGG 150
AGGGTCTAGA CAGAAAAAAT GAATATACCC CAAAAGGCTG AAAAAAAAAA 200
10 CGAGACTTTG ATGGAGAC 218

(2) INFORMATION FOR SEQ ID :1040:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1040:

25 TTTATTATTT TGAATGATTT AATGGTTTTT TACACAATTT ACATCACAAC 50
ATGTAAATTT TAGCAGTAAC ATCTGATTCT AACAGCACAT CATGCTATTC 100
CTTTCATAGA GCCTTCAGAG ATTCAATGCT AAACAAATTT CCTTAGTTGG 150
30 CATCAAGGCA CTGATCACTT TAGAGGCTTT TAAGAAATTA TTTAAAGATG 200
CAAATGCCTC TGAGTGAAGT GTACTATCCC ATCACTGAAG CCCACAGGAA 250
35 CAAGTCCTAC AATTTTAAAA AGGCTCGATG GAAAAATTTT TCAATCCTGA 300
AATCCCCTAG GGAAGGGG 318

(2) INFORMATION FOR SEQ ID :1041:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 base pairs

528

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1041:

ACGTACCGAG CCGTCGTCGC GGTGCTTGAG CTTGAAGGCG AGATAGCCGA	50
10 TGCCGCCGAG GCGGTGGACC GCATCACGGT GGCGCTGACG AACGCGAGAT	100
TCAGCAGCAG CGATGCCATC AATAGCAGCC TGATCGGACG CATGACCGAC	150
15 TCTCCCTGTG AGCGGAGGTT GGGGGGCCGA TCTCCCGCCG GTGCCGGGC	199

(2) INFORMATION FOR SEQ ID :1042:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 300 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1042:

GCCTCTAACA AACTAGGCT GTCCCGGACC ATGGTAATAG AATTGTTTAC	50
30 CTTTATACCA AGAAGGTTGG GAAAGCACCA AAATCTGCAT GTGGTGTGTG	100
CCCAGGCAGA CTTGAGGGG TTCGTGCTGT AAGACCTAAA GTTCTTATAG	150
35 ATTGTCCAAA ACAAAGAAAC ATGTCAGCAG GGCCTATGGT GGTCCATGT	200
GTGCTAAATG TGTTGCTGAC AGGATCAAGC GTGCTTTCCT TATCGAGGAG	250
CAGAAAATTC GTTGTGAAAG TGTTGAAGGC ACAAGGCACA ATGTCTGGAA	300

40

(2) INFORMATION FOR SEQ ID :1043:

529

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1043:

10

GAGACCAGTC TCAAGTGGGA GGGGCTGATG GTGGGAAGCC CTAGAAGAGA 50
GTCTGGGATG AAGCGGCCTC CTCCCTGTCT TGCCCTCCAA AATTGAGTCT 100
GGCCTGATTC CTTTGAGGAG CAAATTTTAC AATCATCCCT CACCCTAACA 150
CACGGTGAAA CTGGAAAACC 170

(2) INFORMATION FOR SEQ ID :1044:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1044:

30

GGCCCCCCT GGGGACTGCT GGTTTCCAGG GGCCACCCCC CCTCATCCAA 50
AAGAAGAATC AAGTTTTGTT TTCCTGTGGT TCCCTTGCTC TCCCCGGCCT 100
CACCTCGAGC TTCCAATTGG GCCCTTTCCC ATGCTTCTAC TTGAGCCCCG 150
CCTGCCTCAC CGTCTGCCTC ACCGCCACCT CCTGCTCAGA GTGAGTGCAT 200
GCATGCCAGA CAGATACACA TATACATACA CACACACACA CACACCCTAT 250
TTTTTTTTTTT 260

40

530

(2) INFORMATION FOR SEQ ID :1045:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1045:

AAATCTATAA TTTTAAGGGC TTAACCTGTG ACTTTAATAA GCTGGAACAG 50
15 TCCACTGAAT GGGTATAATG AATTGCAGTA TATACGTATG ATCGCTTTTT 100
AAGTGATTAT CTTTTCTTTC GTTAAGTCAT GTAAATTCAT AAATTTTTTG 150
GCACTGATGT GTTG 164

20

(2) INFORMATION FOR SEQ ID :1046:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1046:

TCCCTCCTTT CCGAACTGGA GCCCCATCCT CTCCAGAGTA TCCAGGGCTT 50
35 CTTCACTCCC GGGTACCTGC CCTTCGGCCC CTTTTCACCA CAGCTGTGCT 100
ACTGTCAACC AGTCTTTGCT GCATAGGCAT 130

40

(2) INFORMATION FOR SEQ ID :1047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs

531

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1047:

10 GCTTAACTGG AAATTGGAAG GGAAAAGAAG AAGAAACAAT GTAATGTAGC 50
AGTGGGAAGCA AAATTCTCAC AATGAATAGC AGTCTTTCCA GCTTCTTTGA 100
CACGGATTTT CTCATTAGAA AAGACGACTC TCCTGAACTA GGGATGAGTG 150
15 TGAATCTCCA TTCGAGGAAG GGAAGAAGA GCTCGGAGGG TGACAGCCTC 200
CCCCTGAGAG AGCCAGTTGC GTTCATGATT TTGATTCCTT CTCCTCCTG 250
ATGAAGTATC TGCCCAGGAG CCCAGGAGCA GAATA 285

20

(2) INFORMATION FOR SEQ ID :1048:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1048:

TAAAACTGAC CTAGAAGCTA TCAGCAACCA CAAAGAGACA GAAGAAAAGA 50
35 CTGCTTCTGA GGCTCTCTCA TGGAACCTAC TGATGATGGT AATACCACGC 100
CCAGAAATAA CGGAGTCGAT GATGATGGCA ATGATGACGG CGATGATGAC 150
GGCACTGATG ACCCCAGGCA CAGCGCGAGT GATGACTACT CAACACGAGC 200
40 CAGGTCTTTC TGAAGGCCGA GAGAGCTAAA TAA 233

532

(2) INFORMATION FOR SEQ ID :1049:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1049:

ACTTTAATTT ATTTCGGATG CCGGAATTGT GCCCAGAGTT TCTCCTGAGC 50
15 TTGATTCCAT AGCTAGCAGC TTCAATCCTT CGCAGCTGCG GTGCGTTCTG 100
AACTCTGAGC TGTCTTTTCC TGACAGGCAC TTTCCATAGC ATCTGCCTGC 150
TTAATTCCTC ACGACTCAGA AATGTTAACG GCACTGTCGA GTGCTGTGAT 200
20 CATTTTGCTT TAACTATGTA AAGCTTTATG CCCTTCGAGA AGCTTATTTT 250
GAGATAGAGC TAGAGAAGAA AAGCAGCAAA ATTCGGTCGA TAC 293

25

(2) INFORMATION FOR SEQ ID :1050:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1050:

AAAACATAC TTTCATTCAA AAGAAGAGCT GAATTGATGC TTGAGTTACA 50
GCACAAATCT ATTATTAGTG AATGAAGTAT ATTCTTGGCA GATAAATACC 100
40 AGATCAAAAG TCCTGTTTCA GTAATTGAT TAAACTGTAG AATACTAAAA 150

533

AATAAGTTAT TTCTACAGAA ATCTTTGAAG GGAGCAAAAA ATCAAATCAC 200

AGTATATACC TAATGGCTA 219

5 (2) INFORMATION FOR SEQ ID :1051:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1051:

AGCGACCGGC GCTCAAGTGG AATTCCGTGC AGTGTGTTGAT TTTTCGTTTT 50

TGCGATAGTT TACTGAGAAC 70

20

(2) INFORMATION FOR SEQ ID :1052:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1052:

ATTCCTGACC TGTGATATCG GCCATTAGAG CCTTTCAAGA ATGGTACCTC 50

35 CTGCCGATGA TTTTTTTTAA AGCCTTAATG AAGAGAGTGT CCTCTGACTC 100

CTTCCAGAGA AGATAGGATG TGAGTGAGTA AGTTATGTAT AATAATTTTA 150

TCTCAAAATA ACCACGTCCT TGATACCATT CCCTGTATAC CAAGGAAGGG 200

40

TATT 204

534

(2) INFORMATION FOR SEQ ID :1053:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1053:

ACTAAACACA GCACTGAGAA TTCTCCTCTT TTTACAAAAA TGACAGACTT 50
15 AAGAGAGGGC ATGGAACAGA TTAAGAGAAT TAACACGGAG AGGAGAGCAG 100
AGGTATAAAA GGTATCCAAG AAAAGTAAAA CATACAAAGG CAATTCAAAT 150
CAAAGTGAGC ACTGCCTATA TACAGACAGA AAGCGAGTCC TCTATGAAAC 200
20 CATACCCGAC AGAAAGTACC GGAATACCAC CGACACTGAT GTCTTCCAAA 250
CG 252

25

(2) INFORMATION FOR SEQ ID :1054:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1054:

AAATCAGGAA ATTGTACATG TTAACAAAAT AGTATAACCA TGCATACATA 50
CATCTGCTTA TTAAACACTG AAGTAAAAGA ACTAATCCAG TTTGCAGTCT 100
40 TTAGAGGTGT TTAGTATTTT ACTCCGTCTT GATGGAAGCA CTTTGAATGC 150

535

TTGCATGGAG ACATAAAACT GAATATTTAA TTGACAATAG ATCATGCGCC 200
TGTATTTATA AA 212

5 (2) INFORMATION FOR SEQ ID :1055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double.
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1055:

ATAAACTGTG CTAATAAG TTTTATTTT ATCAATATAA AAGCTGTAAA 50
AAAACTGAGG AGAAAGCAGT TGCCAAAAG ATGAAAGAAA AACAACATAG 100
20 AAAACCTTTA AAACAGGCAA AAGTCAGTTC ATAATAAAGT AACTCATCTC 150
AC 152

25 (2) INFORMATION FOR SEQ ID :1056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1056:

AACAGATCCT CAGTTTCTCT GGAGACACCC CCAATTCTCG GGTGAGTGTT 50
GAAACCTGAC AACTGACTGT TAGCCTTGTC ATCATCCTCA TTGGAGATGG 100
40 AGATGTTGTA GTCGGAGCCT CATTCCTTCC GGGGCACTGT TTCTTCTAAT 150

536

GGCAACCATC AGAGCCTGTC TGGAAACAGC CTGCTGCCTT TGCTAGGGGG 200

GCAAA 205

5 (2) INFORMATION FOR SEQ ID :1057:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1057:

GAGAGAAGAG CGCTTTTCTG GGCTCTTGGT TACTCCGTCA GAGACTTTGC 50

CCTTTGTCTG TTAAATACA CTGGGAGCCA GAGCTGATTC CCCACCTGCT 100

20 GCTGTGGTTT TCCGCTTAAC ACAGGAGAGA TGAGTTGGTC TGGTATATTT 150

GATAGCAGGT TTAAATGA ATCC 174

25 (2) INFORMATION FOR SEQ ID :1058:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1058:

TATTTGATGG TCCATAAGAC TTTGTCAAAT GTAAACCTAC AGTTTGATAA 50

GCTTTAAAT ACCATGTTGA CAGCATTTTG AATTGTTTCA TAGACGTACT 100

40 TATTTAACTG ATGCGAACAT TCACA 125

537

(2) INFORMATION FOR SEQ ID :1059:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1059:

TTATCTTACA ATTCTACTTC CCAGCATCCT GAAATTTTCA AATACTGTCT 50
15 TAGTATATTA AACTCTTTTG AAATAGATAA CAAAAGCACC ATGGGAGTCC 100
GTTGAAAAC TAGGTTTGTT CCTTCTAAAA TTTCTAAGTC CTCATTATG 150
ACTATAAAGA AAAAAGGTTT ATCAATTCAA AAAAAAATCC TGATTCTTCA 200
20 AAATA 205

(2) INFORMATION FOR SEQ ID :1060:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1060:

35 ATCTCACAGA TTCTTTTTC CAGATTCATT CATGTTGAGT GAAAGAAGCC 50
AGATGCAAGA GTCCACACCA CATGATTCTG TTTCTATACA ACTTAATTG 100
AAAAC TAAGC AATACTTACA GAAGTGAGAA TAGTAGTTGT CTCAGGGTAG 150
40 GTGAGTGTCA TGAAGGGAAT CTTATACGTT TGCTAAAAAT GTTTATAAT 200

538

ACTTGGATTT TGGGTCTA 3CTGGCAGG GGAAGGGTA CATTGCAAA 249

(2) INFORMATION FOR SEQ ID :1061:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1061:

15 TAGCACATTG CATCCCAAGA GCTGTAGTCA AAATCCTCAA AATCTGATGA 50
AAATGGCATA CTACACTAAG GAGGATTTTT TGGGCATTTT CCATTCATAT 100
GCAGAATCAG TGGTTGAAAA AGGAGAAAGA GAGATTTTCT TTACAAAAGC 150
20 TCCTGACCCC ATTAACATCT TATCTATAAA TCTGATATGT TCCTGACTCC 200

(2) INFORMATION FOR SEQ ID :1062:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1062:

35 GCGCACAGCT GAGAATCTCC GGTCTTGTCT CACTTTGGAC TGGGACAGTG 50
GATGCCCATC TAAAAGTTAA GTGTCATTTC TTTTAGATG TTTTACCTTT 100
ACAGCCATAG CTTGATTGCT CAGAGAAATA TGCAGAAGGC AGGATCAAAG 150
40 ACACACAGGA GTCCTTTCTT TTGAAATGGC CACGTGCCAT TGTCTTTCCT 200

539

(2) INFORMATION FOR SEQ ID :1063:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1063:

TATCAAATCA TGAGTTGAAA GATTTTGACT ATTGAAAACC AAATTCTAGA 50
15 ACTTACTATC AGTATTCTTA TTTTCAAAGG AAATAATTTT CTAAATATTT 100
GATTTTCAGA ATCAGTTTTT TAATAGTAAA GTTAACATAC CATATAGATT 150
TTTTTTTACT TTTATATTCT ACTCTGAAGT TATTTTATGC TTTTCTTATC 200
20 AAATTCAAAT CTCAAAATCA CAGCTCTGAA TCTTAGAGTA TCATAA 246

(2) INFORMATION FOR SEQ ID :1064:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1064:

35 CCCTCATGTG CCAGTTCGGT CTGCCTGCAG AGGCTGTGGA GGCCGCCAAC 50
AAGGGCGAGT GGGAAGCGTT TGCAAAGCCA TGCAGAACAA CGCGCAAGTT 100
TGAGCAGAAA GAGGGCGACA CGAAGGACAA GAAGGACGAA GAGGAGGACA 150
40 TGGAGCCTGG ACTGAGCCAC 170

540

(2) INFORMATION FOR SEQ ID :1065:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1065:

CTCTCCCCCA CAGGTTCTCA GCAGTTACTA AGATGTCCCC TGATTCATT 50
15 GACCTCTGTG TGTCTTCAGT CCTTGACCCT TTAAGGCTCC CTGGTGCCAG 100
AATGTCTGCA GCTGTAGGAT CAAAGACCCT TGGGGGAAAA ATCCATTCTC 150
AAAAGAGAGG AAGATGGGGT G 171

20

(2) INFORMATION FOR SEQ ID :1066:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1066:

GAGTCTATAT CCCTTACTCA GTGCAGTTCT CAAAGTCCTT TGTATGTCGT 50
35 ACAGGATCAC ATCTGTACAT ATCACACTCT TGTGGGGTAA GCCCAGAAGC 100
TCATACACAG CTCATGGGT TTA CTTTCCC AAGCACTTCC TCCCTCCCTG 150
CAATATCTCC CCAGCACTTT CTGCTTCCTA TCAGCTTTC CTTTTTCAA 200
40 C 201

541

(2) INFORMATION FOR SEQ ID :1067:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1067:

ATCAACCGGA GGTGAAATGA AATACCGTCA ACCTGTGCAT GAGTTTGTGT 50
15 GAACTGAATG TGTGTGCATA CACATAAGCA TGTGTGCGAG CGCAAATGTG 100
GCGTCTCCAC AGCATGCGCA ATCCATGAGT CTGTTTCTAA CGCGCGCGCG 150
C 151

20

(2) INFORMATION FOR SEQ ID :1068:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1068:

ACTGTGTCAT GTCAGGTTAG ATCTGAATCT CTAGGAGAAT AGCTTTTTTG 50
35 ATCTGTTTGC TCCTTTGAGT CTCCTTTTA CTTTACAACT AGAAAACCAA 100
TCGCATACTT CACTTCTATC GCTTCCAGAT ATGGCATATT TTTCTTAGGC 150
TACCGTTGAA ATTTAGCATA ATATTTCTCC CTTACCTTTA CGTCCTTTTA 200
40 AAAAAATAGG ACTATAGTAA GTCCTCCGTG TCGGTGGCAT GTTTTTGGAA 250

542

ACTGACTTTA AAGAAAACAT ACA

273

(2) INFORMATION FOR SEQ ID :1069:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1069:

15 CAATCTTGCT TATAAAATAA GAACACCTTT CAATTAAGTG AGTGGGTCAT 50
TCCTGGTGCA ATTGTGATTT TTTTITAGCC AAAATGAATG GCAAACCTCTA 100
TTTAGAGCAA AGTAAGTATT AGAAAACCCT AGGAACTCTT AATCAACGTT 150
20 TATTACACTT TTATAAAGGC AACTACGCG AAAGAGCCC 189

(2) INFORMATION FOR SEQ ID :1070:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1070:

35 TTTATTCCAC TGGAGAAAGG GGATTGAAAA TCAGTTAGAA CCAATGTATT 50
TCTTGCCCCA CGGAACACTA TTCCTATAAG ACAGCTGAAA GAAGCTGCCG 100
TGAGGAGCTC AGCTCCAAAC ACAGGATCAG CACCTCGCAT AGGAATTCCC 150
40 ATGAATCAG ACTTCTCATC CCGTTTTATC AGAGTGCATA TACGTCCTAC 200

543

TTAAGGAAAA GTAAACAGT CATTTACGAA AGAAAGTCAA TCTGTATCCT 250

AAGCATTTTA ATAAAAAGTC AGAAGGAATT 280

5 (2) INFORMATION FOR SEQ ID :1071:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1071:

AGAACCGAAG CCTGCAGAGA GGCCATTCTG ACAGGCTGGG AAATGTAGCC 50

TACCGCCAGA AGCTAGAAGC AAGCACTTCC TCCTAACCGA GTTTTTGAAA 100

20 GACTAAGGGA AAGAGAATAG AGAAGGGATA TTCCCATCTA CCGGGGAAAA 150

GATGCGCAGT AACAAACCAT CTAGGGAGAC AGCCTTCTAA CAG 193

25 (2) INFORMATION FOR SEQ ID :1072:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1072:

AAAGCACCTT CCCCTCGCTG AGCTCCAGGG GGCCAGATA GGCCACGCGC 50

AGCTCCAGCA TCTTGGAGAG CTGCACGTCA TCTGCCGCGT CGTAATCCTC 100

40 CACTCTGCAG CCATAGGCCC CACTCTGGCC CCGGGTCACT CCCTCCAGGG 150

544

TCAAGTTCCC CTCGAGATTC ACATC

175

(2) INFORMATION FOR SEQ ID :1073:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1073:

15

AGTGCCCTAC TCTTTTCCCA AGAAGGGTCA AAGCCTACAA TATCATCAGG

50

GGGCATGAAG CACATTAATT TGCAGTGGCT GCTTCATATG AGGAGGTATG

100

GTGGACAGGC TAATTTTTCCTTGAAAATGT GGCTTCTTCA ACTCCTTTCA

150

20

AATTTAGGAT GGAATACTTC CTGAAATAAA AACTGGGCTT TATGCAGGAT

200

TCTCTTTGAA AATTCTTGTA TGTCCAGAAC AAAAGATAAA ACTAATTGTA

250

25

TTCCTCACAT TCACAATCCC CATTGGTCTG AAGTCACGTG ACACAGAGCA

300

TCTATATAGC ACATAGTGTT TAAAGACTAA TGAATGCAA

339

(2) INFORMATION FOR SEQ ID :1074:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1074:

40

ATTAATTATG CGGTCCTCCT CCTGGCAGCT GGACACCAGT TTGAATCTTC

50

545

CTTTGAGCTC CGGAAAGTTG GTAATTACAA CTTGATATTT CTACATGGAA 100
ATCAAGAAAC TCGGACCCAA CTTGGTGCAA AGACGGATCT CCGCCGATTC 150
5 TGACGGCTCT CCAGGTTTTG TC 172

(2) INFORMATION FOR SEQ ID :1075:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1075:

AGAGTAGGAA GAGGGAGGGG AACAGGCATC TAAGATAGAC TTTCTCCATC 50
20 TGTTGGGAGC CTGGGCAAGT AGGAAAGAAG CCTTTTTCAT ACACTTCAGT 100
CGTATGACTG AGCTGCTTGG CAGGGCACTG GAAACGACGA ACTCGCGCAG 150
25 CCTGCAAATG AGACCACTCT CATTTCTCAG TTTCGATTTG ATTCACTCAC 200
TAGTAGTTAG GTAAATACGA GCTCTATGTG ACTCAAGGAA TGTCAGGCTG 250
GGGCAGGTGG CAAAAGCTAC AGTGATCGAA ATTCACGTTG CTA CTGATG 299

30

(2) INFORMATION FOR SEQ ID :1076:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1076:

546

5 GCCCTCATCG GCGATACTGG AGGTTTCGCTT TCTCAACCCT GTGGGCTTCA 50
 CCCCAGACAC GCCCTGAATC GTTTCATGTT CCAGCATGCC TGAGACAATC 100
 ATCGACTGAA GGATGTTCTC TAACACCCGC ACGAGCTGCC GGCAGATCTG 150
 AATGCCCAAG TCACTCAGCA CCTGCCGATA CTCAGCCAGG TCAAAATCGG 200
 CGAGGTAGTG CTCATGCCTG GCGAGACGTG TTGTGCTTAA TGAAGCCCTA 250
10 TCATTCGAAG TATTGCTATG AGCAGTGC GA AAA 283

(2) INFORMATION FOR SEQ ID :1077:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1077:

25 ACCAATCAAG TACTACTAAAT TAGAATATTT TTAAAGTATG TAACATTCCC 50
 AGTTTCAGCC ACAATTTAGC CAAGAATAAG ATAAAAACTC GAATAAGAAG 100
 TAAGTAGCAT AAATCAGTAT TTAACCTAAA ATGACATATT AGAAACAGAA 150
30 GATATTACGT TATGCTCAGT AAATAATCAA GAGATGGCAT CGCGTAAGAA 200
 GGAGCCCTAG ACTGAAAGTC AAGACATCTG AATTTCAGGC TGGAAAAC TA 250
35 TCAGTATGAT CTAAGCCTCA GTTCTCTNGT CTGCAAAATG AAAGCAC 297

(2) INFORMATION FOR SEQ ID :1078:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

547

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1078:

AAATCTTTTAA TCAATCGAAA CCTTAATAAT TAGGACTGAT AATAGTGATC 50
AGTGATTGAA CCTTTATTAT TTACCAGCTA ATATAGTAGG CCCATAAATA 100
10 GGTATATCA TTCGTAGTCA CAATAACCAC ATACATCACA CACCATGACG 150
TAGCGCTACT ACCCATACCT GCTAGCAGTC AAGGTTGAGA TAATCATAAC 200
15 ACGCCCAACA TCTCATTGAT AGTGAGTTAT CCAAACAGGA ACAATCTCAA 250
GTTTATATCT AAAGCCCATG TTCTTTTGCT TAATATTAGA G 291

20 (2) INFORMATION FOR SEQ ID :1079:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1079:

AGTCACAGCC CCTATACTCC CTCTACACAT TAACCACAAC ATAAGCGGGG 50
CTCACTCACC CACCACATTA ACACCACGAA ACGGGTAATC TAACACGAGA 100
35 AAACACCCTA ACGTTCATAC ACCCCATACA CCATTA 136

(2) INFORMATION FOR SEQ ID :1080:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

548

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1080:

CCAAGGTCGC CTGTGTGCTA GTCACGACCA TTAGGATCCG AAGAAGAGAT 50
GATGACTACC CTAAAAGTAA GGTCTGTGAA CAGCCTGTAA TGGGACGTGA 100
10 GCTGCGGTAT TAAAAAATC AAGAATGGAA GCGTTCCTCA ATTGTCGTTG 150
AGAATCATAC CAACACGGCA GATGCAACCA TGAAAAACGC AGCTGCGTAT 200
15 CGCGCGTTTT TCATGGTTCG CATCTGCCGT GTATGCAATG ATTCTCAACA 250
CACATTGGAG TCACGCGGCC TGCCTAAGAG TATGAAGGTC TTCCTGTAAA 300

20 (2) INFORMATION FOR SEQ ID :1081:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1081:

GTTAATGGTT TTTTCATACA TATGAGACTG AGCGGTCAAA GTTTTACTAA 50
AGTCTTTATG ATCTTTAATT AATACTCCAA GACATCCGAG TTTGGCAGAT 100
35 ATTGGATGAG ATTTGTTTTG CTCCTTACTT TCTTTGTATA CAGCCAAGCC 150
TGAAAATCTC TAGACATTTG CTGAAATTGA TGAGAGCATG CACAGGACGA 200
CTGAAGGTGC TGGACATGA 219

40

(2) INFORMATION FOR SEQ ID :1082:

549

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1082:

10

ATTTTGGGAA AGTGAGCATG AAGAAGGGAC TCAGAGCTGC CAGGTACCCG 50
AGTCTCAGGC TCTGACATCT CTTGGGGCCC CCTTCTGCCA CAACTTCTTG 100
15 CCACTTCACG GACTTGAATT ATGTCCCGCG CCTAAAAAAA AGATTGGCCT 150
GCAGCACAGG CGTGTATCCT CTCCAAAAG CTGCTGCTCA TTTCTGGCCC 200
CATCTGCTGC TATCTTTGCC AGTCAGCCAT CACAGTTTGG CATCATCAGA 250
20 GTCTCAGCTA GAGGGAGCGT GTCATTTCTG CCTTAGTGGT TTGCCTGCGA 300
CCTGACCAGG GCAAGACCAG CTGGGATGTC AAGTGACATT TTGGGAACTT 350
25 GTCGGAAGTT 360

(2) INFORMATION FOR SEQ ID :1083:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1083:

40

CATACATATG AGACTGAGCG GATCAAAGTT TTACTACAAG TCTTTATGAT 50
CTTTCAATTA AATACTACTCC AAGACATCGA GTTTGGCAGA TATTGCGCCC 100

550

GCCGTTTTGC TCTTCTTATC TTTGTATCCA GCCAAGCCTG AAAAGTCTCT 150

AGACATTTGC TTGAAATTTG ATGAGAGCTT GCACAGGCCG ACTGAAGGAT 200

5 GCCGGACATG ATTCTCTGCT TTCTGGTTCA AAAAAAAAAA AAAGTTCCAG 250

(2) INFORMATION FOR SEQ ID :1084:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1084:

TNCTAGATAC NTCCCTCTGT CTCACATTCA TAGTGTGTTT TGTCTAGTG 50

20

TATGAAGTCT CACNCAAGGA AAGTGTNCAG GCAGAGTTTG GGGAGAGTGA 100

AAAAAGTGAA TGGCCTATAT NTGCTCTNTT GGGTGNTCCA NCCATTATTG 150

25

GGGTGAACCC TTTCAGCTTT TTCCTAAAAA TTTGAAAAGA NTTTTTTAAA 200

AAATTAAAAA GAGGATTTTT AAAAGGAATA TCTTGTTCAG AATTNTTTAA 250

GTTTTAATAG G 261

30

(2) INFORMATION FOR SEQ ID :1085:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1085:

551

	GCAATCCATA AGTGTCTTA TCTACAAAGT GAAAAGTTGG ACAAGATATT	50
	CTTCATGATC TTTTTCGATT TTAAATGTC ATGCAATTTT AGAGAAAAGC	100
5	TGAAGGGTCA CCCAATATGG CGCGACACCA AAAGACAAAT ACGAGGACAA	150
	TCACTTTTTC ACTTTCGCA AACTATGCCT GGACACTTCC TTGGCGAGAC	200
	TTAATACACC AGACAAGAAC AACTATGAA TGCGAGACAG AGGGAGACAG	250
10	AGGCGAAATA	260

(2) INFORMATION FOR SEQ ID :1086:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1086:

25	AAGACGTGGA TTTGCTGGAA GACACGGATT TCCTGGAAGA CCTGGATTTT	50
	TCGGAAGCTA TGGATTGAG GGAAGACAAG GATTTTCTGG AAGACATGGA	100
	TAATCTGGAA GACATGACTT TGTCGGAAGA CGTGGACTTG CCGGAAGACA	150
30	CGAATTCCT GGAAGACCCG GATTTTTCGG AAGCTATAGA TTTAAGGGAA	200
	GACAAGACGG ACT	213

35 (2) INFORMATION FOR SEQ ID :1087:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

552

(xi) SEQUENCE DESCRIPTION: SEQ ID :1087:

5 TCCCAGGCAC CCGCTGAATT TCTGAGGCCT TGCTTAAAGC TCAGAAGTGG 50
TTTAGGCATT TGGAAAATCT GGTTCACATC ATAAAGAACT TGATTTGAAA 100
TGTTTTCTAT AGAAACAAGT GCTAAGTGTA CCATATTATA CTCGACGTCG 150
10 ATCATTCTC AGTCCTATTT CTCAGTTCTA TTATTTGAGA ACCTAGTCAG 200
TTCTTTAAGA TTATAACTGG TCCTACATCA AAATAATAGA AATTACGTTT 250
TTTTTT 256

15

(2) INFORMATION FOR SEQ ID :1088:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1088:

TTGCTTAGAA CGGAGCTAGC AAGACAAAAA TACTTCAGTT GGCATCTCCC 50
30 TTAAAGCACA TCCCCAAACG CGGGTCCTGG CCCCAGACAG GGAGACCAGG 100
GCTCTGACAG TGACAGGTTC TTCCCTCTGA AAAAAGAATA GAAGAGGAGC 150
TCCTCCCTAA CCCACAGATT CCCAGGGCAG ACCCTGGGAG GAGGTGCTGA 200
35 AACACAGAAG AGAGTGTGTC TTCCCCAACC TCTACCAGAC AGTAGAGAAA 250
CTGAGGCGAG AGGC 264

40

(2) INFORMATION FOR SEQ ID :1089:

(i) SEQUENCE CHARACTERISTICS:

553

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1089:

10	GACCTGGAAT TTGTTTTCGT CTGTTCACTA GACTCCGATT TCAGAATATG	50
	TCGGAATTTT AGACTCCGGA ACTTTTGAGA ATGTCATTAC AGGAACTTTG	100
	TTTACATACC GAGCTGTTAG CCCAGTCAC TGGGTCCGAA ATTACGCCGA	150
15	TACCGAC	157

(2) INFORMATION FOR SEQ ID :1090:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1090:

30	GCATATACCA AAAAAGGACA AACAGATAGA AGAGTCATCT CAGTGTGTAA	50
	CGAGGAAAAG ATTTATCTCC CATCCTCTGA TCCTCCATAT GATATCTGAT	100
	AGCGAAGATG ACAATAACCC CTTGACTCTT CACGAAAACG CGATGAGAGA	150
35	GAAACTTGAA AAGTCAGAAA ATAAGTTCAT ACCGCAATTA ACCTTTTGGT	200
	CAAGTAATGG AACTTTTGA CTACTAGTGT AAGTCAAAAG ACAAAGGACT	250
40	CCAGCAAGAT GAGAGATTTT TCTATTTTGT AACGAGTAGT CCACCGATCG	300
	TCATCAAAGA GAGAGAATGA ACAACTACGA AAGTTTAAGG GAAAAAAAAA	350

554

AAAAAACATA GATGTT

366

(2) INFORMATION FOR SEQ ID :1091:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1091:

15

GGTCTGAATC ATGAAAAGC CCATAAGAGA GATACAGTGA CTCCAGTTTC

50

AATCATATTA CAGGAGATGA ATCTGTTGCT CTCCATTTT GCTCTTGTC

100

CACCATATGA AGACATCAA AAACACTTAA GGATTCGAGA AAGAGAACAT

150

20

CTTTTGTTAA AGAAGAGAAT AAGATTTTGG AAGAAAAGT AATAGCAAAT

200

TTGAAGAAGA AACAAGTTAC GTAGGGACGA GAACAAGTAA ATAAGGCCTA

250

25

TCATGCATAT CGAGAGGTTT ACATTGATAG AGATAATTG AAGAGCAAAT

300

GGACA

305

(2) INFORMATION FOR SEQ ID :1092:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1092:

40

AAATGGAAGT TGAAGTGAAGT GTGGTTTCCA GTACAGGGCA TCTGGCCACC

50

555

TTCACCTCAG TAAATACTGC TGATCGACTC TCTCTGGCTC TGGCTGTCCT 100
GCCAGAGACA GCCAAACACA GGAGACATGA CAAATTACTA TCATCTTTTG 150
5 CTTCTTTATT TTTATTATTA TTATTTTCT TTTGTGGAG AACAGCGTCT 200
TGCTGTATTG CCCAGCCTGA TCTCAAACCTC CTGGGCG 237

(2) INFORMATION FOR SEQ ID :1093:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1093:

20

AGAAATTTAT TGCCTCACAG TTCTGGAGCC TGAAGTGCA ATATCAAGGT 50
GGAGACAGGG TTGGTTTCCT CTGGAGGCCA TAATGAAAGC ATCTGTTCCA 100
25 GGTCTCTGTC CTGGCTTGT AGAAACACGC ATTCTTCTGG TGGATCCACA 150
CAGTCTTCTC CATGTGTATC CTTCTTCAG TTTCCCTTAT AGGACACCAG 200
TGATGTCAGA TTAGGGATCG AACCCAACAA CCTCATTGA AGTTACTCAC 250
30 CTGTTTGAAA ACCCTATGTC CAAATACAGT TATAGTGTA GGAAC TAGGA 300
CTTAGGGCTT ACAAATATGG AGTGGGGCAT CATCCAGACC ATACCATTTA 350
35 AATTGCAGGG TTTCTCTCCA ATGTGAGTTA CACACACA TTAAGGTTTG 400
TGGGATTCAG AAAGGTATAC 420

(2) INFORMATION FOR SEQ ID :1094:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs

556

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1094:

10	GTTTCTTGGG TAACCTCCCC TCCTTAATCC TTCTGGCATA GGCAGACTCA	50
15	CAGCAGGTAC CCAGTAGAAG GTAAGGTGGC TGATCATTTT TCCATAGGAG	100
	GTCTCCATGG CACACAGGGT AGAAAGTGCA TTCTGTGAAT TAGAGGCAGC	150
	AGAGCATGGC AGCTAATGGA AACTGGCTCT GGGAGGTCAA AT	192

(2) INFORMATION FOR SEQ ID :1095:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|---|
| 20 | <ul style="list-style-type: none">(A) LENGTH: 228 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear |
|----|---|

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1095:

30	AGAGAGCTTA ATAAGACCTA ACTACAGGCA AACCTGACTG GAACGTGAGT	50
	ATCTGTGGTC TGGTGTGGAA ATAGCTCTCT AGCCCCATCT CCCTCCTCCC	100
	ATTGTCCACC CCCATCCTCC TTACCACGAA ACACATTTTT CACCAGCATT	150
35	GCCAAACCAC TTGGGATTCC TGC GCATGGC TTTGCTTAGT TTGCTCTTCT	200
	GCTTCTTGGA TACCTCCTTC AGGAAATC	228

(2) INFORMATION FOR SEQ ID :1096:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs

557

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1096:

ATTTTTTATG GAAAAAGGGG GATAATGCAA AATAGCAAAA ATTGTAAACA 50
10 AAGTTAAAGA TTATCTTCAT CTAAACCTTA AGCTGACAAT TTA AACACC 100
TTGTGCATAA TGCAGAAAAA AACTGTCCGT TTGACTTCAC TTCATTAC 150
15 ACTGCTCCCT ACGCATGAGA AAGACCAGAT GTCTGGTTTC AGAGTATT 198

(2) INFORMATION FOR SEQ ID :1097:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1097:

TAGAGAGAAG TTGATATATG AAGATAGGGT GGACAGGACT GTGAAGGAGG 50
30 CTGAAGAAAA ACTGACTGAA GTGTCACAGT TTTTCTCTAC AAAACTGTGA 100
CACTTCAGTC AGTTTTTC 118

35 (2) INFORMATION FOR SEQ ID :1098:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

558

(xi) SEQUENCE DESCRIPTION: SEQ ID :1098:

5 AAAAGTCACT AAAGTCANTG TGTAATACGA AAACCGAACA CTCCAGCAGT 50
 CCTATTTTAT NTNTTCCAAC CTAGNNCACC CAGGTGACGC NNGGGACTCG 100
 TCNCAGGTGT TTNGNACTTG CCGCCCGACN GGCNAAGG 138

10 (2) INFORMATION FOR SEQ ID :1099:

(i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :1099:

 ACTCCACCAC TGGGNCCGCC ATGTTTTGGG TNGGNGCAAT GCGCTGTCTG 50
 TGAGCGCCAN TCTAATTGTA TTNGGACTGC ACGGGTCCGT AACTGACTG 100
25 ACACTGGGCT ACCTCGCCCG AAAATGNGAA CACCGCTCAA TATCGNTGCG 150
 G 151

30 (2) INFORMATION FOR SEQ ID :1100:

(i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :1100:

 TAGCAATAGG CTATAACATA AGCCGAGGTA TAGGCTACAC TAGCTAGGTT 50

559

CGTGTAAGTA CACTCTATAT TGGCACAACA TAAAATTAAC TAGTGACGCA 100
TTTCTCAGAA TGCATCCCCA TCGTTAAGTG ACACAGACTG TCCCTCATAT 150
5 CACCGGAGGA CTGGNCCAGG ACCTCCTGGC GGCACCAAAA TCCACGAGCG 200
C 201

(2) INFORMATION FOR SEQ ID :1101:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1101:

20

TAGCAATAGG CTATAACATA TACCGAGGTA TAGGCTACAC TAGCTAGGTT 50
CGTGTAAGTA CACTCTATAT TAGCACAACG ATAAAATTAA CTAGTGATGC 100
25 ATTTTTCAGA ATGCATCCCC ATCGTTAAGT GACACATGAC TGTCCCTCAG 150
TATCACTGGA GGACTGGGNC CAGGACCTGA CCTGGTGGTA CCAAATCCA 200
TGAGGCNGNA AT 212

30

(2) INFORMATION FOR SEQ ID :1102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1102:

560

CGGTAGCAAT AGCTATAACA TATAGCCGAG GTATAGGCTA CACTAGCTAG 50
GTTCGTGTAA GCACACTCTA TACNNGCACA ACATAAAATN AACTAGTGAT 100
5 GCATTTCTCA GAATGCATCC CCATCGTNAA GNGACACATG ACTGTCCCTC 150
AGTATTACTG NAGGACTGGN CCAGGACCTC CCTGGGGTAC CAAAATCCAN 200
GAGTGGAAAT TCCANCAT 218

10

(2) INFORMATION FOR SEQ ID :1103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1103:

GTAGCAATAG GCTATAACAT ATACCGAGGT ATAGGCTACA CTAGCTAGGT 50
25 TCGTGTAAGT ACACTCTATA TTAGCACAAC GATAAAATTA ACTAGTGATG 100
CATTTTTTCAG AATGCATCCC CATCGTTAAG TGACACATGA CTGTCCCTCA 150
GTATCACTGG AGGACTGGGN CCAGGACCTG ACCTGGTGGT ACCAAAATCC 200
30 ATGAGCG 207

(2) INFORMATION FOR SEQ ID :1104:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

561

(xi) SEQUENCE DESCRIPTION: SEQ ID :1104:

GGCGTCAAGT GGCCCAATCT AACAGCTCCA GGGTAGCCAC AACCATCGTG 50
5 ATGGATTGCC ATTATTGTGT GCTAGTGGCT AGAGGTAGAC CCAATAGAAC 100
TCTGCCCCAA CAGGGCAACA GCCAAGCTCA ATTCTCCAAG CCCCCTGAAC 150
AGACCTTCCA CATCCAGGAG AAGCTGTTGT TGTCTAGAGC TACTTAGTGT 200
10 CAGAATCCAG GCCAGCTTGG CTGCTTGATG CGACTGGCTA TAGGATTNGN 250
GTGNAGGCC 259

15 (2) INFORMATION FOR SEQ ID :1105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1105:

ACATGACCCC TTGGA CTGAA GCGCTCAGT AGTAAAGGAG TGTCATGCAG 50
GTCAACACAT GTCGCACATG GACCACAAAG CCTGCCACCA GCAGGATGCA 100
30 CGGGGACTTC TGGGAGGGGG TGGACAGGAT ACTTATCTGT GACTGGAATG 150
CAGGCGAGAG GCGGAGAAGA GAGTGAAGGA TAACTCATAG AGGGGGCAGC 200
35 ATTTGTTTCG NGTTGAAAGA GGCAGAAAAT 230

(2) INFORMATION FOR SEQ ID :1106:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

562

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1106:

ACATGNCCTG GACTGAAGGT GCTCAGTTAG TAAGGGAGTG TCATGCAGGT 50
CAACACACGT CGCACATGGA CCACAAATGC CTGCCACCAC AGGATGCACA 100
GGACTTTTGG GGGGAGTGGA CAGGTATTAT TGNGACTGGT GAGGTGAGAG 150
GTNAGAGGGG GCT 163

15 (2) INFORMATION FOR SEQ ID :1107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1107:

ACNTGATGAT TGCCATTATT GTGTGCTAGT GGCTAGAGGT AGACCCAATA 50
GAACTCTGCC CCAACAGGGC AACAGCCAAG CTCAATTCTC CAAGCCCCCT 100
GAACAGACCT TCCACATCCA GGAGAAGCTG TTGTTGTCTA GAGCTACTTA 150
GTGTCAAATC CAGGCCAGCT TGGCTGCTTG AT 182

35 (2) INFORMATION FOR SEQ ID :1108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

563

(xi) SEQUENCE DESCRIPTION: SEQ ID :1108:

5 CCCCTGGACT GAAGGCGCTC AGTAGTAAAG AGTGTCATGC AGGTCAACAC 50
ATGTCGCACA TGGACCACAA AGCCTGCCAC CAGCAGGATG CACGGGGACT 100
TCTGGGAGGG GAGTGGACAG GATACTATCT GTGACTGGAA TGCAGGCGAG 150
10 AGGCGGAGAA GAGAGTGAAG GATAACTCAT AGAGGGGGCA GCATTTGTTT 200
CGNGCCTTGA AAGA 214

(2) INFORMATION FOR SEQ ID :1109:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1109:

25

ACATGGCCCC TGGACTGAAG GTGCTCAGTT AGTAAGGGAG TGTCATGCAG 50
GTCAACACAC GTCGCACATG GACCACAAAT GCCTGCCACC AGCAGGATGC 100
30 ACAGGACTTT TGGGGGGGGT GGACAGGTAT TAT 133

(2) INFORMATION FOR SEQ ID :1110:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1110:

564

GCATGACCCC ATGGCACTGA AGGTGCTCAG GTTAGTAAGG GAGTGTTCATG 50
CAGGTCAACA CATGTCGCAC ATGGACCACA AATGCCTGCC ACCAGCAGGA 100
5 TGCACGGGGG ACTTCTGGGA GGAGAGTGCA TAGGATACTT GTCTGTGACT 150
GGAATG 156

(2) INFORMATION FOR SEQ ID :1111:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1111:

20

GGCGCTCANT GGATCCAATA CACCAGACTC CCGGGAGCGA AAACGCCCCG 50
AGGTGCCTCA AAGAACTTAA AACAGAACTG CCATTAGACC CCACAATCTC 100
25 ATNAAGGATG TTATAGATAT ATCCAAAAGA AAATAAATCA TTCTTCAAAA 150
AGACACATAC ACTAACACGT TCATGGAGCA CTATTCACAC AGCAAAGACT 200
CGATCAACTC ACACACTCAT GAATGCGGAT CGAAATAGAA GATGTGGTAT 250
30 GCATACACCA CGAAATACTA CGAGCCATAA AA 282

(2) INFORMATION FOR SEQ ID :1112:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

565

(xi) SEQUENCE DESCRIPTION: SEQ ID :1112:

TAATTAGTTT AACCAGTGTG GAAAGCGTTG TAGGGTCTCA AAGACTNAAA 50
5 ACAGAACTGC TTAGACCCCA CAATNTTANG AGCGGATGTT ATGATATATT 100
CAAAAGGAAA TAAANNGNCN TGTNAAAGAC CATAACNAT NGTCCATCGG 150
AGCCCGTATN CACGCAGCTT GTCATAACTA T 181

10

(2) INFORMATION FOR SEQ ID :1113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1113:

ATCCAATGAC ACCAGACTCC CGGGAGCGAA ACGCCCGCAG GTGCTCAAAG 50
25 AACTTAAAC AGAACTGCCA TTAGACCCCA CAATCTCATN AAGGATGTTA 100
TAGATATATC CAAAAGAAAA TAAATCATTG TTCAAAAAGA CACATACACT 150
AACACGTTCA TGGAGCACTA TTCACACAGC AAAGACTCGA TCAACTCACA 200
30 CACTCATGAA TGC GGATCGA AATAGAAGAT GTGGTATGCA TACACCACGA 250
AATACTACGA GCCATAAAAG GCGAAATC 278

35

(2) INFORMATION FOR SEQ ID :1114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

566

(xi) SEQUENCE DESCRIPTION: SEQ ID :1114:

ACCTGCAAAC TTTTCTGTA AAGACCAGAT AGTAAGTATT TTATGCTTTG 50
5 TGAGCCATAC AGTTTTTGTT GCAACTAGTC AACTCTCAAC TNACGTGGAC 100
AGCATGTAAA GAACGAGAGT GACTG 125

10 (2) INFORMATION FOR SEQ ID :1115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :1115:

GTAGCGACCG GCGCTCATGG AATTCGGGA CCTGCAAAC TTTTGAAAG 50
ACCAGATAGT AAGTATTTTA TGCTTTGTGA GCCATACAGT TTTTGTGCAA 100
25 CTAGTCAAAC CTCAAACAC CGTGGACAGC ATGTAAATGG ATGGGAGTGG 150
CTGCCGG 157

30 (2) INFORMATION FOR SEQ ID :1116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :1116:

CCTGCAAAC TTTTCTGTAA AGACCAGATA GTAAGTATTT TATGCTTTGT 50

567

GAGCCATACA GTTTTTGTTG CAACTAGTCA ACTCTCAACT NACGTGGACA 100

GCATGTAAAG AACGAGAGTG ACT 123

5 (2) INFORMATION FOR SEQ ID :1117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1117:

ACCTGCAAAC TTTTTTTGTA AAGACCAGAT AGTAAGTATT TTATGCTTTG 50

TGAGCCATAC AGTTTTTGTG CAACTAGTCA ACTCTCAACT CACCGTGGAC 100

20 AGCATGTAAA TGGATGGGAG TGGCT 125

(2) INFORMATION FOR SEQ ID :1118:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1118:

35 ACCTGCAAAC TTTTCTGTA AAGGACCAGA TAGTAAGTAT TTTATGCTTT 50

GTGAGCCATA CAGTTTTCGT TGCAACTAGT CAACTCTCAA CTTACCGTG 100

GACAGCATGT AAATGGATGG GAGTG 125

40

(2) INFORMATION FOR SEQ ID :1119:

568

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1119:

ATTAAGCTTG ACACATCTGT GTTATCACGC ACTGAAGACA GGAAGCAGTT 50
 CACTGAGTCA GCTGGCTTCC AAGCTTACAC AGAAGGCGAT AAGTCACTAT 100
 CAAAGAGCCA ATGAGAATCT TCTTATAGAA TAACCTGGGC CCAAGTGA 148

(2) INFORMATION FOR SEQ ID :1120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1120:

AGAATAACAG AGCCAAAGGA CTAATAAAAT CAATGAATCN TGGTGAGACT 50
 AATCAAGAAA AAATAGCACC AACAACAATG AGGAGAAAAT GGAAAAAGGG 100
 CAGAGTATTT CAATGATTAC GAGAGGGCAA ACCAATCAAC GAATGATTCT 150
 TAAGCCTTCA GTTGCCCTG TAAGCAAACCT GAAGACGTGC AAGTCATCCT 200
 TTGCCCTGGG AGAGTTAACT TAACCCACAG GGACAACTAG 240

(2) INFORMATION FOR SEQ ID :1121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs

569

(B) TYPE: nucleic acid
(C) STRANDEDNESS: doubl
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1121:

AAATGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AAGAATCCTG 50
10 GTGAGACTAA TAAGAAAAAA TACACCAACA ACAATCCGAG AAAATGGA
AAGGGCAGAG TATTTAATGA TACGAAGATG GGCAAACCAA TCAATGAATG 150
15 ATTTTAAAGC CTTACAGTCT GCCCTGTAAG CAACTGAAG ACGTGCAAGT 200
CATCCTTCGG CCCTGGAGAG TTAACGTTNC CCAAGGGGCA ATGAGAAGGG 250
ACAG 254

20

(2) INFORMATION FOR SEQ ID :1122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1122:

AAACGAGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TCAATGAATC 50
35 NTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT GAGGAGAAAA 100
TGGA AAAAGG GCAGAGTATT TCAATGATTA CGGAGAGGGC AAACCAATCA 150
ACGAATGATT CTTAAGCCTT CACGTTTGCC CTGTAAGCAA ACTGAAGACG 200
40 TGCAAGTCAT CCTTTGCCCT GGGAGAGTTA ACTTAACCCA CAGGGACAAC 250

570

GAG

253

(2) INFORMATION FOR SEQ ID :1123:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1123:

15 AAATGGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AATGAATCCT 50
GGTGAGACTA ATAAGAAAAA ATACACCAAC AACAAATCCGA GAAAATGGAA 100
20 AAAGGGCAGA GTATTTAATG ATACGAAGAT GGGCAAACCA ATCAATGAAT 150
GATTTTAAAG CCTTCACGTC TGCCCTGTAA GCAAACCTGAA GACGTGCAAG 200
TCATCCTTTG 210

25 (2) INFORMATION FOR SEQ ID :1124:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1124:

AAATGGGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TTAATGAATC 50
CTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT CAAGAGAAAA 100
40 TGGAAAAAGG GCAGAGTATT TAAATGATTA CGGAGACGGG CAAACCAATC 150

571

AACGAATGAT TCTTAAGCCT TCATGTTTGC CCTGTAAGCA AACTGAAGAC 200

GTGCAAGTCA TCCTTTGGAC CCTGGGAGAG T 231

5

(2) INFORMATION FOR SEQ ID :1125:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1125:

AAGTCCCATC AGCAACCCGT TTTTACCAG ATGTCACTCA AGAATGCGCC 50

20 CGTGGCCCTC CAGTTCCTGC GCACTAAGAG CGTCCCGCT 89

(2) INFORMATION FOR SEQ ID :1126:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1126:

AAGAAACCCG AGACMCCAAC TAATCCCAGA ACAGCTAAAA CCAATAAAGA 50

35

ACCAAAACTT CACGACCACT TTCCTGAGGA CCCTGCTGAG TGCTCATGAC 100

ACCAATACTG ACAATTGTAG CGGTAATACA TACAATGATT TAATAAGCCT 150

40 ATGCTACTGG ACACATGCCC ACACAATAAT ANTCANRTGT NTYGTTAGGC 200

CTACT 205

572

(2) INFORMATION FOR SEQ ID :1127:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1127:

GCAAGGCCTG GCCGACAACA CCCTTATTGC TAAAGTAAAT AATGNCGCGC 50
15 GGGGCCTGGA CCACCCTCTG GAAGAAGATT GTACCTTGGA GCTTCTCAAG 100
TCTGAGGATG AGGAAGCTCA GGCAGTGTAT TGGCGCTTTA GTATCACATA 150
A 151

20

(2) INFORMATION FOR SEQ ID :1128:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1128:

GAGCACCCCA GCCCATAACA CAGAACTCGT CCCCCTACCC CCCTCAGCAA 50
35 GCCGGAGAGG CTAGCCCAAG TAATCATAAY AACAGCCGCC CGAGAGCAGC 100
CCCAGTAGCA GCCCCATGGC CGGGCGGAAC ACCTACATCG ACAACCTCAT 150
GACAGACGAG ACCTGCCAGG ACGCAGCCAT TCGGGGCTGC AAGGCCTCRC 200
40 CCTTCGTCTG GGCCGCCGTC CCCGGAGAAA CGCTCGT 237

573

(2) INFORMATION FOR SEQ ID :1129:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1129:

GCCTCGTGGA AGTGACATAG CCTTTAAACC CTGCGTGGCA ATCCCTGACG 50
15 CACCACGTGA CGCCCAGGAA AGACAGGGCG ACCTGGAAGT CCAACTACTT 100
CCTTAAGATC ATCCAACATAT AGGATG 126

(2) INFORMATION FOR SEQ ID :1130:

20

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1130:

GCCATCTTCT GTAACAAAAT AAATAGTGTC AAGCACTAAA TATATGCATG 50
AATGCATCAG CAATAAGATG ACAATCAAAG AATGCTGTGA AGATTGGCAT 100
35 CAAGATGTTA GCAGCATACT GCAGGACTAG GCTTAGAAGC CTACCTGCAG 150
TTTATTTGCA AGGATTTTTTC TTTCGRGGGC GGAGGGGAGA GAAAAGTAAA 200
TGTGCTAACT TCGGATACTT GCCCTTATAA AGAATTCCTT YGTATC 246
40

(2) INFORMATION FOR SEQ ID :1131:

574

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1131:

10 CGAGGATCCG GGTACCATGG CAAGTCTCAT GAGGCTATTT ACCGAATTTA 50
TCCTCTGTCT GACCATGATT TTTCCCTCA AATAACAACCA CTCCTCGACT 100
15 TTTCACCCTC AAAGTATAAA AAGTATGAAA NATAAACAAG CTCTTGCACT 150
GTACACTTAG AAGTGTACAA TTAAAGCATT ATAGAGCTAT CTACACACCG 200
ATAAATCCCA TCGAATCTTG AATAATCCAT CAATACGTAG AACGCAAGGG 250
20 TGCAGACAGA ACTAAAACCA ACT 273

(2) INFORMATION FOR SEQ ID :1132:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1132:

35 GAGGATCCGG GTACCATGGT CTGTATATCT GTGCTTCCAC TTCTCGGAGG 50
TGCTAGAGGG GAGGCTGTCC TCTGGTCAGG AGAATCCTAT TCAGTGCTCC 100
CTTAGACATT CTTCCAGGCA GGATCAAACCT CAAAGGAAAA GGAATTTGTG 150
40 AAGCAAACCA TGGCTTTGTC ACAGTAAAGT AATTGTCACT CTCAACCCAG 200

575

AATGTGTGAA GCGCTGCAGG GAGAAGCTTC TCTTCCAGGA GAGCAATANA 250

AGCCAATGTA TCTGACCCTT GCTTYGATGA GAGTTAATAA TAAGTATTAT 300

5 ATTTCTGTTT GTTAAAAAGT TCAGAATTT 329

(2) INFORMATION FOR SEQ ID :1133:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1133:

CCCCGAGCTA GTTGTCCCGA CCTG 24

20

(2) INFORMATION FOR SEQ ID :1134:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1134:

GAGGATCCAC AAACCATGGA AACTCTCGC GGCTGCCACT CCCCATGAC 50

35 CACCCTACAG GCCCTAACCC CAGCCCCTCA CGTTATCGTC CAGCCACAAA 100

TAGCTGCCGC CCTGAGATCT CCACCTCAGA CCCTCTCCCG AAGCCCACAG 150

CGGCCCCCTGC CGGGCACCCC AGCTTCCTCG CAGGCACCAA AAGCGCAGTT 200

40

CCAGGAATCT CTACCCTAGA GTGATCCGGC GCCAGTTGCC AGTTAAGGGA 250

576

CCAAACCTCG CCAGAAGGCT TCTTTTCGGG TTGATCGCCA TCTATTY

297

(2) INFORMATION FOR SEQ ID :1135:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1135:

15 GCCGCTTTAC TGCTCAGTTC GGAGCTACCG CTCGAAAGC AACAAAAAAG 50

CNTTTGCAAA TGAAACGAGA TTGCTGAATT GCGTACACCG AGA 93

(2) INFORMATION FOR SEQ ID :1136:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1136:

30 CGAGGATCCG GGTACCATGG AGCTTCACAC GGGTCTTCTT GGTCTCAGGG 50

TTGTGGGAGA TAACGGTGGC ATAGTTCCTT GATGCCCGGG CCAGCTTGCC 100

35 ACGGTCTCCA GGCTTCTCCT CCAGGCAGCA CACGATTGTA CCCTCAGGCA 150

TGGTGCCAC AGGGAGCRCA TTGCCAATGT TGAGCTGGGC CTTCTTGCCG 200

CAATACACAA ACTGGCCCGT GNGAATGCCC TCGCGGGCAA TGAACAGTTC 250

40 CGCCCGCTTC TTAAACCAAG ACAGATCCCG GAAGGCCGCC TGGGCAAGGG 300

577

GCCCCTCRAA CCCGGGGCTA TACACGTCAA AATC

334

(2) INFORMATION FOR SEQ ID :1137:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1137:

15 CGAGGATCCG CATACCATGG CCCCCATCTT ACGAGCCCTT ACTCCTCATG 50
ATGAAGAAAC TCCAAACCCT TTGACAGCTC CTCGGGGTNA AACCTGGNAY 100
AAAGCTGACT GACCAGGCTC CATGAAATCT CCCATCTCCA TRATGTACCT 150
20 CCTTGRTGCC ATCTCTATAT AAAGMGAACC AGTCCTAAAA TCAAACACT 199

(2) INFORMATION FOR SEQ ID :1138:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1138:

35 CGAGGATCCA AATACCATGG CGCTCCCTCC TCCCGAGCGC CGCTCCGCGT 50
GGCACCCGGC TCGCTCCGAG TTCAGGCTC GTGCTAAGCT AGCGCCGTCG 100
TCGTCTCCCT TCAGTCGCCA TCATGATTAT CTACCGGGAC CTCATCAGCC 150
40 ACGATGAGAT GTTCTCCAAC ATCTACAAGA TCCGGGAGAT CGCGGACGGG 200

578

TTGTGCCTGG AGGTGAAGGG GAAGATGATC AGTAGGACAG AAGGTAACAT 250
TGMTGACTTG CTCATTGGTG GAAATGCTTC CTCTGAAGGC CCCGAGGAAG 300
5 AAGG 304

(2) INFORMATION FOR SEQ ID :1139:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1139:

20 GAGGATCCGG GTACCATGAG AAACCTTTGAA GCCAGAGATT TTAAACAATC 50
AAGGCACTTG AAAACATTAA GTATATGTAC AAATGTGCAA GTAAACAAA 100
CAGCTGTACC AACGAGTAAC AAAGAAACAG TAAATCTTCA TCTTAACAAC 150
25 CTTTAATAGT TATCTAAATG CAGAGTTTGT TTATGAAATG AACCAAAGCA 200
GTTTGTTCATT TCTTACTATA AAATACCGAA AATAAAGTGC AAAACTTAGC 250
CACTACTGGC TAAAGAAACT AAGTAAA 277
30

(2) INFORMATION FOR SEQ ID :1140:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1140:

579

CGAGATCCGG GTACCATGGC CTCCTACAGG TGCCGTGGAG CCACGCCCAA 50
AAGAGAGCTC CCTGAGAAAC TCGTTGATGC CTTGCTCACT GAAGGAGCCT 100
5 TTTAGCAGAG CAAATTTTCAT CTTGCGTGCA TTGATGGCGG CCATGGCGGG 150
GTACCCAAAC CCTCCAATTC CCAACGCGGT CTCAAGTTCA GACTGGGCTC 200
CAGCTTCT 208

10

(2) INFORMATION FOR SEQ ID :1141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1141:

CGAGGATCCG AGTACCATGG CCTCGAACTG AGCATCAATA TATTCTACTG 50
25 CCAGCTTATA ACTGTCATCT TTATTCATAT GGTCTCCAAA TCCCACGATG 100
TCAACAATGG TTAACCTCAG CCGTACATTG CTTTCCTGAA GCTCATAACT 150
TCTGGCTTTT AACCGAACAC CTGGTTCATT GTGAGTAGCT GGGTCACTTT 200
30 TAAATTTGGT GTTGAACAAA GTGTCCATTA ACGTGGATTT GCCAATGCCT 250
GTCTCACCAA TACAAAGGAT GTTG 274

35

(2) INFORMATION FOR SEQ ID :1142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

580

(xi) SEQUENCE DESCRIPTION: SEQ ID :1142:

5 GCCTGCACAT TGACTGTGGG AAAC TCGGAA ACAAGCTCAC ATCTCCCCGT 50
GGGAAACCTT CTAGCAACAG GATGAGTCTG CAGTGAAGT GAGTTGCCAC 100
CTTCCTCTAT GCGGAGGTCT TTGTTGTGTT GCTTCTCTGC ATTCCCTTCA 150
10 TTTCTCCTAA AAGATGGCAG AAGATTTTAA AGTCCCGGCT GATGGAGTTG 200
TTAGTGTCTT ATGGTAACAC CTTCTT 226

(2) INFORMATION FOR SEQ ID :1143:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1143:

25

RGGRTCCRNG TGCCRTGGGG YNTNNCTAGR CRGCRGGYAA GGTCCACCRC 50
TGRRCRCGNTG NCNGTGAGGR CRTGNRGGNC CRTGCGAGTG GGCTTACCGN 100
30 TAGGTTCGGG AATGACCTTG CYMACGNCNN YGACAGCTAA GTRGRNGCRG 150
GNANGRTGNN GTGGAGRG 168

(2) INFORMATION FOR SEQ ID :1144:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

581

(xi) SEQUENCE DESCRIPTION: SEQ ID :1144:

CGAGGATCCA AATACCATGG AGCTGACAAT GTCAGCTCAA TTTGAAGTAT 50
5 TCTTGAGGGA CCTTTTGCTC ATAGGCTTTA ATTCTGTCTG TGACTTTTGC 100
CAGGATTTGA GGAAATCGAC TGCCTTCACT CTTCCCTGAA ACTTTGAAGT 150
CCACATAAGG GCTTTCTCAT CAAATGGCAG AAATTATAAT TTATAAACCT 200
10 AAACAACCTT ATAGTGTTTT CGCTTTGAAT TGTATGAATT CTTAGAACTG 250
AGAAGT 256

15 (2) INFORMATION FOR SEQ ID :1145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1145:

AAACACAAGG CTAAAAGTCA CTAAAGGTGA CACAGTACCA ACCCCGGGAA 50
GGTTGAGTTC TGTGCTGCTA CCTTCTACTG ATGGCGAATA GACTATTCTG 100
30 TACCCTGTGA TGGGAGCCTG GGGTCTGCTC CAGCAAACAA CAATCGAGGT 150
GTAATCAACT TGGTCCACAG TCGGGTCAGG AGGG 184

35 (2) INFORMATION FOR SEQ ID :1146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1146:

5 CGAGGATCCG GGTACCATGG CCCAAAGAGT GAATGATGTA TCCCAGGGCG 50
CAGTCCACAA CTTGCGCAGT ACCTTCCCAG ATGACAGCCT CACTGGACCG 100
ATTTCCATCC ACGAAGATGA TGCTAAGAAG CACCATGAGC AGACCCAGCT 150
10 TGGGTGAGTC CTTAGTCGTT CCCAGTATGC CTGCATCAGT GGGCTCTAAG 200
GTGCTGAGAA GAATGCACAA G 221

(2) INFORMATION FOR SEQ ID :1147:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1147:

25

CGAGGATCCA AATACCATGG GAGTCAAGCA TGCCTCGATA GCCACAGATT 50
TACAAGAATT ACCTACAGTT TGCTTCTTNG AATCGACATG CAAATCTGCT 100
30 TAAGGATTCT CACATTCAGG ACAGAGAACA AATTTTTTAA TGAATCCATC 150
CAACAGGTCT TGNAGTTTAT TCGCCTCATG AGATCCATTG ATAATGGAAC 200
RRTMATTCTT AACANCAAAC NGMGMTGNN NTCCCRNCTT ATAACCMAAA 250
35 GATNT 255

(2) INFORMATION FOR SEQ ID :1148:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid

583

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1148:

	CGAGGATCCA GGTACCATGG ACGATTACACA GCCCCTGGCC ACTGGCCATT	50
10	TCCAGTGGTA GGGAGCACAC TGRTCACATT CGAGACCCAC CACGTTGAGC	100
	AGACAAAGGC AGCCTCCACT CTCCTCGTCA CTCAACATGT ACCTCCGTCC	150
	CCCAGGATGT TGTAGTTATA GCAATAGCAG CCCTGCGGTT GACGTAGGTG	200
15	AGTCGGTGAC GCCCGATTTG GATCGGGTGT	230

(2) INFORMATION FOR SEQ ID :1149:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1149:

30	GTGCCGTTGG TCCTGTGCGG TACTTAACC AAGATGCCTG AGGAAACCCA	50
	GACCCAAGAC CAACCAATGG AGGAGGAGGA GGTGAGACG TTCTCCTTTC	100
	AGGCAGAAAT CGCCAGTTG ATGTCATTGA TCATCAATAT TACCNACTAG	150
35	AACAAAGAGA TCTTTCTGAG AGAGCTTATT CAAAATACAT TAAATGTATT	200
	GGACAAAATT CGATATAAAA GCT	223

40

(2) INFORMATION FOR SEQ ID :1150:

(i) SEQUENCE CHARACTERISTICS:

584

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1150:

10	CGAGGATCCG AGCACCATGG AGAGACTATG ACGCTCAACA AGAATCACTC	50
	GGAGGGCGAC GGAGTGATCG TCAATAACAC CGAGATTC CTAATGCCCT	100
	ATGATCACGT GGAACATAACA TCAATGACA TGAAGAACGT GCCAGAAGCC	150
15	TTCAAAGAGA CCAAGAAAGG CGCTGTCTAC CTTACTTCTC ATTGAACCAT	200
	CTTTATGTCC AAGAACAAGG ATCGGATGGG TATTTCTGTA NGCTATTGTA	250
20	NMTRAGGRMA GNCTGNAAGG TM	272

(2) INFORMATION FOR SEQ ID :1151:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1151:

	TGAGGATTTA TAGATTANAG CTAGAGTTCA CATTTTATGG ATTACAACCA	50
35	AAAAAACCT GAAAAAGAAA AAAAACAAAA AAGCTCAAAA GCAATCACAA	100
	GGATAGTTGA ATCCCTCTTT AAACCCCCAA AGCAACCCCC	140

40

(2) INFORMATION FOR SEQ ID :1152:

(i) SEQUENCE CHARACTERISTICS:

585

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1152:

10	AAGGATCCGG GTACCATGTA TTCCCCCGGT ATCAGCAGAG GCGTGTACGG	50
	GCACTGCTTT AAAACTGGGA AGGAGGAAGA CGAGGCCAGG GAGCCGGAGG	100
	GTCACCAAGG TAGATTTCCA GCAGCCTAGT CCAGCTGAAC GCTTTCCAGC	150
15	CTTGCTTTTT AGCAGCTTTG AGGAAAAGTA TAGTGATCCG GATGTGAAAC	200
	TTTCATTG	208

(2) INFORMATION FOR SEQ ID :1153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1153:

30	CGAGGATCCA GGTACCATGG GGTGGATCCG CCGGGCATAG CCACCCTGGA	50
	TGGTGGCCAT GGTGAGGCCG ATGAGGAAAA ACATCTTCCC CTGCTGTAGG	100
35	CTACTGAACT GGAAGCGCTG GTGTGTGAGG AAGCTCAACG TGCACTCCAG	150
	GCCCAAGAAC AGGAAGAGGT AGAGGAAGTA GACTMGGCCC AGGCGGCCAG	200
40	GCTGATGAAT TGTCTCCAAA GGGTGAGACC TGGCCACGAG CCATANCCCA	250
	GAMGCCNMAC AGGGCTRGGG ACTG	274

586

(2) INFORMATION FOR SEQ ID :1154:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: "SEQ ID :1154:

GAGGATCCAC CGACCATGGA AACTCTCAA TGGCTGCAAC CACCCCGTGG 50
 15 CCCCCCTACC AGCCCCAATC TCCAAACCCC GCACGTCGAT CATGACGCCA 100
 CCAACAGCTG CAGCCCCTGA GATCTTCACC TTAGACCCTC TCCCGAAGCC 150
 CGCAGCCGCC CCTGCGAACC CTCCAACCTG TTCACACGCG CCGAAAGCCT 200
 20 ATTCCCAGGA CTCTCTGCCC CTACGTGACC GNCCCTAGCT GCTAGTCGAG 250
 AATCCGAACT CCGCTCC 267

25

(2) INFORMATION FOR SEQ ID :1155:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 231 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1155:

CTCAAACCCC GNTTCCCCC TAATAAGAGC AACTAAAAA CTTCTGATAA 50
 CCACAATAAA AGCGTGCATT TGAGCACAAT TCAAAAGCCA ACCCCTTCGA 100
 40 AGGNGCTTCT GATGNAAAAG GAGTTATGTT GAACGAAGCA GGAGTTAACG 150

587

CTACACAGTC AAATTGTGGC ATTAGGACGC GCGAGCGGGC TAGCTGCGGC 200

CGTCTANCAA GGCAACGGCC GCCTTTGAAT T 231

5 (2) INFORMATION FOR SEQ ID :1156:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1156:

GCGCGAGCAC AGAGCCTCGC CTTTGCCGAT CCGCCGCCCA TCCACACCTG 50

20 CCGCCAGCTC ACCGTGTATG ATGATATCAC CNGCTCGCC ACCAACRACG 100

GCTCYAACMT GTGCAAGGCC GCCTTCAA 128

(2) INFORMATION FOR SEQ ID :1157:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1157:

35 GCCGCAACAC AACCCAGGGA GACTCAAGNC CACAGGGGCC CCCC GGCTCT 50

GAGGGATTCA CCGTCGCCTC CCGTCCCCG AAGGCCCACA AGGGCAGAAA 100

GGTGAGCCTT ATGCACTGCC TAAAGA 126

40

(2) INFORMATION FOR SEQ ID :1158:

588

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1158:

10 AATAACCATA ACTGCAAAAA CCCAAMCAAA AAAAAAGGGG GAACAAAAAA 50
CCCCAAACCC CCAAAAAAAC CAGAAAAAAC CACAAAAAAA AACCCCTCCT 100
15 T 101

(2) INFORMATION FOR SEQ ID :1159:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1159:

GAGGATCCGG GTACGGGCAG GGTGAGAGCC TGGGGTCCAC CGATAACCGG 50
30 GAGGGAGATG GCGTTCTTGA GCAGAGGGGA TGGGCCGTCC GGGAGCTCCC 100
CCCACACACG GTGGCGGTGC GGGTGAAGTG GAAGGGGAGG TCGAAGGTGC 150
35 CATCTTCTTC AGGCCCCCTCC AC 172

(2) INFORMATION FOR SEQ ID :1160:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

589

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1160:

	GAGGATCCAC ATACCATGGA ACAGCACCAC AAAAATAGCC ATTTTGATCA	50
	TGGTTATTTT CCAGGACCAC ACGATTGACC TACGTCCTG GAAGGCTATG	100
10	TGTCTGTTCT GAGCCTTCCC ACTCTCCTAA AGGGCAGATG AAGATCAGAG	150
	CTTTGACCCT GTGATGCCAT TTAATCAAC CCTGCTTGGT TTTAGAGGAT	200
15	TGCTCCCGTG GGTCACTTGA GGCAGGCTCC ACCTT	235

(2) INFORMATION FOR SEQ ID :1161:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 284 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1161:

	GAGGATCCAC CAACCATAGA AAGTAAATAC TGTATAAAAA GCTCCAGCTG	50
30	TTAGATACAA ATGCAAAACG CTCCTTAAA AACGGCCTGA AAAAAAATC	100
	ACAGACAATG CCAAACTTTA TAGGTCTGTA TTTTCCTTTA TACAAAATGC	150
35	CCTCAAATTA AAAAGTAATT CCCATATAGC AATAAAGTCC ACATCTCTGG	200
	ATTACCTATA ACCGGTATTA TGGGGTGTGT TTATACTGCC TAGAATGTTA	250
	ACCCTCATAA AGCCTTAAAA GTACATTTGT GAAA	284

40

(2) INFORMATION FOR SEQ ID :1162:

590

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1162:

10

GCTCACATAA	ATTTCTTCAC	CGACCCTTTT	CCTTCCAGCT	TCCTTACTAT	50
AAAAAACCCC	ACA	ATA	TGTTTCATCAT	CATCCATACT	100
15	GTCACCATCT	CAATCAGCAG	CAAGTCCTAC	TCTCTGTGGG	150
	TTACCACCTC	TAGGGGCAGA	CCCCTTTTCA	GATATATTCA	200
	ATCCTCCAC	TATAGCGCTT	CGACTTTGTA	TCTTCCTCTA	250
20	ATTCTGTCCG	TTGATAAGTA	CTGGCTCTAA	ACCATGC	287

(2) INFORMATION FOR SEQ ID :1163:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1163:

35	GAGGATCCAA	AAACCATAAA	ATTCATCATC	CCCAGCAGGT	GCNCTAGCTA	50
	TACTTTATTA	CAGCAAARCA	CAACCACACG	CTGAMCTANM	TCGTATAGAT	100
	AAACACCAAT	CATGGGTCGG	CC			122

40

(2) INFORMATION FOR SEQ ID :1164:

591

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1164:

10

GCGCGGGTCT GTCTCTTGCT TCAACAGTGT TTGGACGGAA CAGATCCGGG 50

GACTCTCTTC CAGCCTCCGA CCGCCCTCCG ATTNCCTCTC CACTTGCAAC 100

15

CTCCAAGACC ATCTTCTCGG CCATCTCCTG CTTCTGAAGC CT 142

(2) INFORMATION FOR SEQ ID :1165:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1165:

30

TATTCCCCCG GTATCAGCAG AGGCGTGTAC GGGCACTGCT TTAAAACTGG 50

GAAGGAGGAA GACGAGGCCA GGGAGCCGGA GGGTCACCAA GGTAGATTTC 100

CAGCAGCCCT AGTCCAGCTG AACACTTTCC AGCCTTGCTT TTCAGCAGCT 150

35

TTGAGGAAAA GTATAGTGAT CCGTATGTGA AATTTTCATC GCACGTAGCG 200

GATGAGAATA GAGAACTCA 219

(2) INFORMATION FOR SEQ ID :1166:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs

592

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1166:

10 GAGGATCCAC CAACCATAGA AAGGAAACAA CACTTGGAGT GAACCCGACC 50
CAAGCCACTA CACCCCAGCC TAACCGACAG GTGCTAGACT AATNGTNAAA 100
AACAACCGGA AAATAGACCC GGACGAAGAT CAAAGNTTNT CAATCCAAAC 150
15 ATTTTAGGGG GACCAAGACC CMGGGATCAA AAACAAGGTC CACCACACCC 200
AA 202

(2) INFORMATION FOR SEQ ID :1167:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1167:

30

GAGAAACCTA CCCAACCAAG AGGCGCCCTG CTTTGTAATG ACCTTTACGA 50
AGACACGTCT GATACCCAAC CTGACAGAGG AAACAACAGT AGTCTGAAAG 100
35 GGACAGAATG AGAGAGGGGG CTGGAGAAAG AAATGAATAA ACATGAATGC 150
ATCTGGAGA 159

(2) INFORMATION FOR SEQ ID :1168:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs

593

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1168:

10	CCCTAGACAA GCCACCTGAG GAGAGGCTCG GAGCCGGGCC CGGACCCCGG	50
	CGATTGCCAC CGCTTCTCTC TAGTCTCAG AGGGGTTTCC CGCCTCGCAC	100
	CCCCACCTCT GGAATTGCCT TTCCTTCTCT TCTCCGCGTG TGGAGGGAGC	150
15	CAGCGCTTAG GTCGGAGCGA GCCTGGGGCC ACCGCCGTGA AGACATCGCG	200
	GGGACCGATT C	211

20

(2) INFORMATION FOR SEQ ID :1169:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 211 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1169:

	GGATTTCCGG TCCTGGCTTT CTGATATTTC TAAAATCGAC CTGGAATCAA	50
	CCATTGACAT GTCCTGTGCT AAATATGAAT TCACTGATGC CCTGCTGTGC	100
35	CATGATGATG AGCTGGAAGG GCGCCGGATT GCCTTCATCC TGTACCTGGT	150
	TCCTCCCTGG GACAGGAGCA TGGGTGGTAC CCTGGACCTG TACAGCATTG	200
	ATGAACACTT T	211

40

(2) INFORMATION FOR SEQ ID :1170:

594

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1170:

10 GAGGATCCGC GCAACCATAG AACTCACAAC CCAGCCATAT ACCTCAGACA 50
CAATGGAATG GGCGGAGGTC GAGGTNGACA AACCCCTGAGT AATGTTGGGC 100
15 ACTTCCGCAC CGGAGCTGTT CTTACCTTTG ATAAAGTGGA TGTTATTGCT 150
ATTAATGATC TCTTAACGGA CTTCAACTGT AAAATTNGCA TGATCTAGTC 200
CTATCCACCA ACGNCGAACA ATATGCTGTT GCCAMGATTG AGCACGAGCC 250
20 GTTTGGGCTC AACGGC 266

(2) INFORMATION FOR SEQ ID :1171:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1171:

35 GGCACAACCC ACTTTGAACA ATCATGCTTC AGAAATCTGC CTGACCTTAG 50
CTGCTGCTGC TGCTCACTTT ATTATAGTAT AACTTCGGTA GGCATACTTG 100
GAGAACATAT CCCACATTAG GAATTGATTT AAGCCTGAGA GTTTGAGGGC 150
40 TTTAATCCTT TAAAACT 167

595

(2) INFORMATION FOR SEQ ID :1172:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1172:

AATAAACCTC CCTATCAG TGACCTACTA CCCGCGTGTG CTTATATAAC 50
15 TAATCCAGGA CAACCCACAA AAATTATAGC AACACACAAA CACACCGCTG 100
ACCATAACAT GTGCGTCTTT CAAAGATGCC TTATCAACCA GAGCGATGAT 150
TACTGAGGAT ACGCAACTCA TAAACTCTA CTAAAGCAA CAGGGCAGAC 200
20 GTGCGTCTGT GCCAGTCGTG AATGTGGTGA AC 232

(2) INFORMATION FOR SEQ ID :1173:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1173:

35 GAGGATCCAC CAACCATAGC CCGAAAATGT GGTAAGGGAC CCTCATCTAT 50
CACACAACNC AGGTAAGAAG GCACCCAGCC CCATGGGCCA TAC 93

(2) INFORMATION FOR SEQ ID :1174:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs

596

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1174:

GCCTTTTTTT	ACCCGCCGGA	AGCTACAGCT	TTTGCCCCC	CAAAAAACC	50
10	CCACCCTTTT	ACCCACCGCG	GACCCAAAAA	CAGCAAAAC	100
	CAAGGACCTC				
	TCCCAACCCC	AACCCCTCCT	TTTTGGCCCT	TCCTTCCCCC	150
	CCTCCCAGCC				
15	CACCCCCAGA	CACCTCAATC	CCCCAAAAGG	ATGCCCTAAA	200
	CCTCTCCTAA				

(2) INFORMATION FOR SEQ ID :1175:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1175:

GAGGATCCAA	AAACCATGGC	ATTCATCACG	CCCAGCAGGT	GTCCCAGCCA	50
30	TGACTTACCA	TAGCAAACA	CAACCACACA	CTAACCTGCA	100
	TCGCCTAGCT				
	TACTGATGAT	GATGTCCTGG	T		121

35 (2) INFORMATION FOR SEQ ID :1176:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

597

(xi) SEQUENCE DESCRIPTION: SEQ ID :1176:

AACCAGACAC GCCGACCCGC TGAATC

26

5

(2) INFORMATION FOR SEQ ID :1177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1177:

GAATCGATCT TGACCTGGCT GCCAGGAATA TCCAGCTTGT TACCGACTGG

50

20

TAAAGAATAA GACCGCTGAT CATAGAGTGA AGCTCCAGGA ATCAGAGAGT

100

CTCATAGCAA ACCTCGAAAC TGAGGATGAG ATGGTTACAG ATAAAGCCTT

150

TCAGGATGGA TTMAAGNAMG CAGAGAGG

178

25

(2) INFORMATION FOR SEQ ID :1178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 base pairs

30

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1178:

GGTTAAGTTT TTCATCAAAG ACTCAGGTAC CTATTATCGT TCCCTGGCGA

50

40

AACTGAGGAG AAAAGTTAAT CAACCAGGTT ACTCCCACAG TTTGCCCGTG

100

TGTTATGCAT CAGTTATACA GGTATCCCAC CAAGTTCAAG TCAA

144

598

(2) INFORMATION FOR SEQ ID :1179:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1179:

GACCAGGGAG GAGGTTTAAT CAACTTGGAC CCCCTCCGGC CTAGCCGCCC 50
15 AGGAGGTGCA TTCGGGACAA CCACTAGGTC AGAACGCAGC CTCTCCAGAG 100
TCCTCAGGCT CGACAACGAT TATCCTGCTG CTATCAGCT TTGATTTACT 150
GATCTCGCTG AAAAGACAGA CGCTTTTAGA TACCGAGTCG ATAGGGGGTC 200
20 TGCGGTACTT TTCAGTAGAT AGGTGGTGCT TGT 233

(2) INFORMATION FOR SEQ ID :1180:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1180:

35 CGAGGATCCG GGTACCATGG GCCGGATACA ACGAGCTATC ATTACTGCTC 50
CCATGGCCAA AACCAGCAGT CCCACAATCC CCGTGAAAGG GATGAGGTAA 100
TAGCCCAAGG GGAAGGTATT GTCTGGAACC AGAAGCGCCC GAGCCCCCTT 150
40 CTTGTAGRCA AAGAGGGCGC CCAGGTGCTT GGAGCTNCTN TCCCCAATGG 200

599

AGGTAGACGG GACCAAGATC TGCTG

225

(2) INFORMATION FOR SEQ ID :1181:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1181:

15 TGAGGATTTA AAAATTCTGG AATATCTATG ATTGATCGTC AACTTTATTC 50
GATGAATAAG CTTGATGTGG CCTAGTTTTN NGNNNNNTGG NYATGGTNNA 100
TCNNNTTANT TTTTG GTTG TTGTGNATAT TATNGAATAR AMGAATRGNG 150
20 TTTAGAGTTT GGAAGCGGCN RNCGTARMG NNACTCYACG CTCGCNNCTN 200
TTGNNNNACA GMRGGNTCTC TNGGRTGAGT GGRTNCMGTT GGMGGNNTCN 250
25 NNNTAGCTGN NGNGAGRATC AGCTRGCTTN CTTTNGGCTN GCT 293

(2) INFORMATION FOR SEQ ID :1182:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1182:

40 GAGGATCCGG GTACCATGGC TCTCTCTTTC TTTTTTTTCT TTTTCTTGGC 50
GGATGTGAGA GCTGCCTGAG ATTCAAGGTC ATCCGGCAGC TCAGTCCCCA 100

600

CCACCTCTGT CTCTGGCTCC ACTGTGGCAT CTGCTGTTT TTCTTTCTCA 150
GTCTTCTCTT AGGGAGCTGC CAGAGCTGCC TGGACCTGAG AATTCATTCC 200
5 TTCTGGCTGT TGAGACCCCG TGGACTCCCC TGGATTCCAG AGNNTNATTT 250
NG 252

(2) INFORMATION FOR SEQ ID :1183:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1183:

20

ACGAGGATCT GAATACTCTG GCCTGCAAGT AGAGGCTAAT TCGATGTGTG 50
AAACTGTAGA TTCGGCTTAA GGTAATAGTC ATTTATAGAC TATTCAATAG 100
25 AGTCAGACTG GTCGAGGCTG GTAAGTGTAG CGGAACGGTT GCTGACTGAT 150
ATTGTTAGAG TGAGGCTTGT ACTGGTGTGT ATCCGTAGGT GGTCTGCAGT 200
GT 202

30

(2) INFORMATION FOR SEQ ID :1184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1184:

601

CAGATCCTCA GCTTTCGTGG TTCACAATTT CTTCAGTCTC TTA

43

(2) INFORMATION FOR SEQ ID :1185:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1185:

15

ACCGTCCTTC TGGTTCATCC TAGCAAAAAT CTCACCATCT TCTATCAC

48

(2) INFORMATION FOR SEQ ID :1186:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1186:

30

ACATCATCCG AGTCCCCTCT ACAGTGTTCA TTGTGATCGT TGCATCCCCC

50

TGGTTTGGAA ATAAAATATA AACTGCCCGG CAAGAGATAA AATTGTATTT

100

TTTA

104

35

(2) INFORMATION FOR SEQ ID :1187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 base pairs

(B) TYPE: nucleic acid

40

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

602

(xi) SEQUENCE DESCRIPTION: SEQ ID :1187:

5 CTGGTTCTGT TTCTCGCAGG TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG 50
AGAATCCTAT TCAGTGCTCC CTTAGA 76

(2) INFORMATION FOR SEQ ID :1188:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1188:

20 AATAGGGCGC GATCAACTCT TAACTTTGAG GAGAACCAAC AA 42

(2) INFORMATION FOR SEQ ID :1189:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1189:

35 GGCGGACGTG CGCGCCTTGT CTCGCGGCA CCTGGGCCTG AGGTGCGTGC 50
CTCCCGGGCC CTCGCCAGCT CCAGATGCGT GAGGAGGACT TCAGAAACCC 100
GACTGAGAAG TGGAGCAACC CCCAGGAAGG GCCGGACCTG CCTAAATGCC 150
40 GCCAAGGCCT TTTATTTATG GCTAGTTTGC TCTCGTGAAA TACTAACATC 200
GTTTTAATGG CACTCATCAA GTACGCAAAT GATATGATTT AACCTCGCGC 250

603

AAT

253

(2) INFORMATION FOR SEQ ID :1190:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1190:

15

GAGGATCCAC CAACCATAGA ACGGCCCTAC TAATGAACCA CACAAGCTAG

50

TTGCACCACT ATAGAAACAC AAAACTACAC ATCTATACCA ATAAAAATAA

100

CAACTACTCC AATTGCCCCAT GTGGTATTGT CGCAGACTGA AATGAATTAT

150

20

GAATTTAGGT TGGTTACCAA TATCGGCATA AAATAAACTR TGTAAGGCTC

200

AMTATGTTGA CAGTAAGCTC TTGTCAGGTG TCTAATGAGG TAAAAGCATT

250

25

TT

252

(2) INFORMATION FOR SEQ ID :1191:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1191:

GAGGATCCAA CAACCATAGA GCACATAAAA ACCGCCCAAC GATCTAACTA

50

40

ATATACAACG GCTAACCGGG CCATTCAAAA GCTCGCCCAG ATTAAATGCC

100

604

TGCCGANAGC AAGTACATGG GGAGGATTAC TACTTCCTGG TTGCCAACCA 150

CCCTTCCGGC TGCCCTTGTG TTGACTTG 178

5 (2) INFORMATION FOR SEQ ID :1192:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1192:

GGATCGGCCG TAATCGGTGA GCTCGGTGTC GGGTAAGGGA CCCAGTCCAT 50

CGCCACCAAG CGCCAGGAAT GGGCAGCATA AGGGAAGGCT AAGGAGGACT 100

20 GCAACAGGTT AGGGCCCTGG AGATTGTATT TAGCAAGGGT ACCTGCGNNG 150

NGGGCA 156

25 (2) INFORMATION FOR SEQ ID :1193:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1193:

ATTCTGAATC TTTAATGAAA ATCAGCCCAG AGCTTGTTGT AATACAGACA 50

40 TAACTGCAAG AGCATGCCCA CAGCTTAGAG AGGTTGTACC AAATTTAGA 99

605

(2) INFORMATION FOR SEQ ID NO: 1194

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1194:

NNNNTCCTTC TCCTGCGACA GACA

24

15

(2) INFORMATION FOR SEQ ID NO: 1195

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1195:

TGTCTGTCCG AGGAGAAGGA

20

(2) INFORMATION FOR SEQ ID NO: 1196

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1196:

40

AANNTCTCGG ACAGTGCTCC GAGAAC

26

606

(2) INFORMATION FOR SEQ ID NO: 1197

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1197:

TTNNTCTCGG ACAGTGCTCC GAGAAC

26

15

(2) INFORMATION FOR SEQ ID NO: 1198

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1198:

GTTCTCGGAG CACTGTCCGA GA

22

30

(2) INFORMATION FOR SEQ ID NO: 1199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1199:

GTTCTCGGAG CACTGTCCGA GAG

23

607

(2) INFORMATION FOR SEQ ID NO: 1200

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1200:

GTTCTCGGAG CACTGTCCGA GAC

23

15

(2) INFORMATION FOR SEQ ID NO: 1201

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1201:

CTGTCTGTCTG CAGGAGAAGG AA

22

30

(2) INFORMATION FOR SEQ ID NO: 1202

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1202:

CTGTCTGTCTG CAGGAGAAGG AG

22

608

(2) INFORMATION FOR SEQ ID NO: 1203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1203:

AGCTCGGCTC GAGTCTG

17

15

(2) INFORMATION FOR SEQ ID NO: 1204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1204:

GCGACAGACA GCAGACTCGA GCCG

24

30

(2) INFORMATION FOR SEQ ID NO: 1205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1205:

GATCCGGCTC GAGT

14

609

(2) INFORMATION FOR SEQ ID NO: 1206

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1206:

CCGAGAACAC TCGAGCCG

18

15

(2) INFORMATION FOR SEQ ID NO: 1207

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1207:

GTAAAACGAC GGCCAGT

17

(2) INFORMATION FOR SEQ ID NO: 1208

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1208:

40

CGAGGTCGAC GGTATCG

17

610

(2) INFORMATION FOR SEQ ID NO: 1209

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1209:

CGAGGTCGAC GGTATCG

17

15

(2) INFORMATION FOR SEQ ID NO: 1210

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1210:

TACGTTTCGAC AAGCTTGAAT TCGCGGCCGC TTTTTTTTTT TTTTTTTTTT

50

TTTTTT

56

30

(2) INFORMATION FOR SEQ ID NO: 1211

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1211:

611

GCCWSCGCCG A

11

(2) INFORMATION FOR SEQ ID NO: 1212

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1212:

15 GGTGGCGACG ACTCCTGGAG CCGG

24

(2) INFORMATION FOR SEQ ID NO: 1213

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1213:

30 TTGACACCAG ACCAACTGGT AATG

24

35 In the above SEQUENCE LISTINGS, some sequences are preferred because they fall into the category of sequences referred to hereinbefore which exhibit no more than 90% homology to a human sequence known per se. The preferred sequences in these terms are all of sequences SEQ ID Nos 1 to 1193, EXCEPT FOR SEQ ID Nos:

40 85, 117, 177, 197, 223, 248, 317, 354, 355, 483, 829, 1057, 594, 595, 597, 164, 427, 420, 58, 67, 374, 373, 501, 569, 188, 550, 904, 932, 97, 89, 134, 433, 434, 357, 4, 6, 11, 336, 529, 544, 545, 549, 1037, 847,

612

870, 871, 872, 873, 875, 876, 579, 199, 524, 544, 513, 380, 276, 291,
615, 623, 627, 634, 635, 648, 652, 617, 619, 684, 697, 718, 720, 1127,
1145, 1148, 1164, 938, 587, 589, 588, 241, 243, 335, 61.

5

10

15

CLAIMS:

1. A nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-
 - (a) a sequence selected from SEQ ID Nos 1 to 1193;
 - (b) an allelic variation of a sequence as defined in (a); or
 - (c) a sequence complementary to (a) or (b).
2. A nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof.
3. A sequence as claimed in claim 2 and which exhibits no more than 90% homology to a human sequence known per se.
4. A nucleic acid fragment comprising a portion of a sequence as defined in claim 2 or claim 3 of sufficient size such that a probe of the same size and exhibiting complementarity to said portion can hybridize to said sequence as defined in claim 2 or claim 3.
5. A fragment as claimed in claim 4, wherein said portion is at least 15 bases in length.
6. A fragment as claimed in any one of claims 1, 4 or 5 and encoding at least a portion of a biologically active polypeptide.
7. A nucleic acid sequence as claimed in claim 2 or claim 3 and encoding at least a portion of a biologically active polypeptide.
8. A DNA construct comprising a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7, together with a control or regulatory sequence.
9. A construct as claimed in claim 8 which encodes a fusion protein comprising a known protein and the polypeptide encoded by said fragment or sequence.
10. A construct as claimed in claim 9, wherein the fusion protein encoded is a cleavable fusion protein having an endopeptidase recognition site positioned between codons corresponding to said known

protein and said fragment or sequence.

11. The use of a fragment as defined in any one of claims 1, 4, 5 or
6 or a sequence as defined in any one of claims 2, 3 or 7 to produce a
5 gene.

12. A DNA fragment comprising a gene obtainable by the use defined in
claim 11.

10 13. An expression vector comprising a fragment as defined in any one
of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2,
3 or 7, a DNA construct as defined in any one of claims 8 to 10, or a
DNA fragment as claimed in claim 12, positioned such that that nucleic
acid sequence which encodes the polypeptide corresponding to said
15 fragment, sequence or DNA fragment is in operable reading frame with a
control or regulatory sequence.

14. A vector as claimed in claim 13, wherein said vector control or
regulatory sequence comprises a regulatable promoter.

20

15. Host cells which incorporate as a heterologous part of their
expressible genetic information a fragment as defined in any one of
claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or
7, or a DNA fragment as defined in claim 12.

25

16. A process for the production of a polypeptide comprising
cultivating host cells as defined in claim 15.

17. An antibody directed against a polypeptide obtainable by the
performance of a process as defined in claim 16.

30

18. An antibody as claimed in claim 17 and which is monoclonal.

19. A novel gene product or portion thereof encoded by a fragment as
defined in any one of claims 1, 3, 5 or 6, or encoded by a sequence as
35 defined in any one of claims 2, 3 or 7, or encoded by the gene
comprised in a DNA fragment as defined in claim 12.

40



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(21) International Application Number: PCT/GB93/01467 (22) International Filing Date: 13 July 1993 (13.07.93) (30) Priority data: 9214857.6 13 July 1992 (13.07.92) GB (71) Applicant (for all designated States except US): MEDICAL RESEARCH COUNCIL [GB/GB]; 20 Park Crescent, London W1N 4AL (GB). (72) Inventors; and (75) Inventors/Applicants (for US only) : SIBSON, David, Ross [GB/GB]; 37 Grimsdells Lane, Amersham, Buckinghamshire HP6 6HF (GB). GROSS, Jacqueline [GB/GB]; 47 Boxmoor Road, Kenton, Middlesex HA3 8LH (GB). HADFIELD, Kathryn, Mary [GB/GB]; 5 Carlisle Terrace, St Ives, Huntingdon, Cambridgeshire PE17 4PQ (GB). HOWELLS, David [GB/GB]; 77 Puttocks Drive, Welham Green, Hatfield, Hertfordshire AL9 7LW (GB). STARKEY, Michael [GB/GB]; 27 Creasy Close, Abbots Langley, Hertfordshire WO5 0HS (GB). KELLY, Maria [IE/GB]; 24A Oxford Road, Ealing, London W5 3ST (GB). SHAW, Diana [GB/CA]; 342 Glacier Hall, University of Calgary, 2500 University Drive NW, Calgary, Alberta T2N 1N4 (CA).		(74) Agent: BIZLEY, Richard, Edward; Hepworth Lawrence Bryer & Bizley, 2nd Floor Gate House South, West Gate, Harlow, Essex CM20 1JN (GB). (81) Designated States: AT, AU, BB, BG, BR, BY, CA, CH, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, US, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 31 March 1994 (31.03.94)
(54) Title: HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW (57) Abstract This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.		

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INTERNATIONAL SEARCH REPORT

International Application No.

PCT/GB 93/01467

I. CLASSIFICATION OF SUBJECT MATTER (If several classification symbols apply, indicate all)⁶

According to International Patent Classification (IPC) or to both National Classification and IPC:

Int.C1.5 C 12 N 15/11 C 12 N 15/62 C 12 P 21/08
C 07 K 15/28 C 12 Q 1/68

II. FIELDS SEARCHED

Minimum Documentation Searched⁷

Classification System	Classification Symbols
Int.C1.5	C 12 N C 12 Q C 07 K

Documentation Searched other than Minimum Documentation
to the extent that such Documents are Included in the Fields Searched⁸

III. DOCUMENTS CONSIDERED TO BE RELEVANT⁹

Category ¹⁰	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
Y	SCIENCE vol. 252, 21 June 1991, LANCASTER, PA US pages 1651 - 1656 ADAMS, M. ET AL. 'Complementary DNA sequencing: expressed sequence tags and human genome project' see the whole document ---	1-19
Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA vol. 88, March 1991, WASHINGTON US pages 1943 - 1947 PATANJALI, S. ET AL. 'Construction of a uniform-abundance (normalized) cDNA library' cited in the application see the whole document --- -/-	1-19

⁹ Special categories of cited documents : ¹⁰

"A" document defining the general state of the art which is not
considered to be of particular relevance

"E" earlier document but published on or after the international
filing date

"L" document which may throw doubts on priority claim(s) or
which is cited to establish the publication date of another
citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or
other means

"P" document published prior to the international filing date but
later than the priority date claimed

"T" later document published after the international filing date
or priority date and not in conflict with the application but
cited to understand the principle or theory underlying the
invention

"X" document of particular relevance; the claimed invention
cannot be considered novel or cannot be considered to
involve an inventive step

"Y" document of particular relevance; the claimed invention
cannot be considered to involve an inventive step when the
document is combined with one or more other such docu-
ments, such combination being obvious to a person skilled
in the art.

"&" document member of the same patent family

IV. CERTIFICATION

Date of the Actual Completion of the International Search

08-10-1993

Date of Mailing of this International Search Report

01. 03. 94

International Searching Authority

EUROPEAN PATENT OFFICE

Signature of Authorized Officer

ANDRES S.M.

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)

Category	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No.
Y	<p>NUCLEIC ACIDS RESEARCH vol. 18, no. 19, 11 October 1990, ARLINGTON, VIRGINIA US pages 5705 - 5711 KO, M.S.H. 'An 'equalized cDNA library' by the reassociation of short double-stranded cDNAs' cited in the application see the whole document ---</p>	1-19
Y	<p>NATURE vol. 355, 13 February 1992, LONDON GB pages 632 - 634 ADAMS, M. ET AL. 'Sequence identification of 2,375 human brain genes' see the whole document ---</p>	1-19
Y	<p>GENE vol. 81, 1989, AMSTERDAM NL pages 295 - 306 AKOWITZ, A. & MANUELIDIS, L. 'A novel cDNA/PCR strategy for efficient cloning of small amounts of undefined RNA' see the whole document ---</p>	1-19
P,Y	<p>WO,A,9302214 (MEDICAL RESEARCH COUNCIL) 4 February 1993 see the whole document -----</p>	1-19

INTERNATIONAL SEARCH REPORT

International application No.

PCT/GB93/01467

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos. because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos. because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos. because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see PCT/ISA/206 mailed on 29.11.93

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-19(all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.